GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 2, 2004, 09:52:57 ; Search time 40 Seconds
(without alignments)
767.445 Million cell updates/sec

Title: US-10-066-500-9
Perfect score: 609
Sequence: 1 MIVFGWAVFLASRSLGQGLL.....QNVDGLVLDTLAVIRTLVDK 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1070241 seqs, 262374223 residues

Total number of hits satisfying chosen parameters: 1070241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	609	100.0	117	10	US-09-946-374-6	Sequence 6, Appli
2	609	100.0	117	12	US-10-081-056-6	Sequence 6, Appli
3	609	100.0	117	13	US-10-066-500-9	Sequence 9, Appli
4	609	100.0	117	14	US-10-002-796-9	Sequence 9, Appli
5	609	100.0	117	14	US-10-066-273-9	Sequence 9, Appli
6	609	100.0	117	14	US-10-066-494-9	Sequence 9, Appli
7	609	100.0	117	14	US-10-066-269-9	Sequence 9, Appli
8	609	100.0	117	14	US-10-006-856A-6	Sequence 6, Appli
9	609	100.0	117	14	US-10-066-211-9	Sequence 9, Appli
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16	609	100.0	117	14	US-10-006-117A-6	Sequence 6, Appli
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ALIGNMENTS

RESULT 1
US-09-946-374-6
; Sequence 6, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C1
; CURRENT APPLICATION NUMBER: US/09/946,374
; CURRENT FILING DATE: 2001-09-04
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; Sequence 6, Application US/10081056
; Publication No. US20040043927A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P.Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235P1C1
; CURRENT APPLICATION NUMBER: US/10/081,056
; CURRENT FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/219,556
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; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 6
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; TYPE: PRT
; ORGANISM: Homosapiens
US-10-081-056-6

Query Match 100.0%; Score 609; DB 12; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-58;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
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; Sequence 9, Application US/10066500
; Publication No. US20020177165A1
; GENERAL INFORMATION:
;  APPLICANT: Avi J. Ashkenazi
;  APPLICANT:  Kevin P. Baker
;  APPLICANT:  David A. Botstein
;  APPLICANT:  Luc Desnoyers
;  APPLICANT:  Dan L. Eaton
;  APPLICANT:  Napoleone Ferrara
;  APPLICANT:  Sherman Fong
;  APPLICANT:  Wei-Qiang Gao
;  APPLICANT:  Hanspeter Gerber
;  APPLICANT:  Mary E. Gerritsen
;  APPLICANT:  Audrey Goddard
;  APPLICANT:  Paul J. Godowski
;  APPLICANT:  Austin L. Gurney
;  APPLICANT:  Ivar J. Kljavin
;  APPLICANT:  Jennie P. Mather
;  APPLICANT:  Mary A. Napier
;  APPLICANT:  James Pan
;  APPLICANT:  Nicholas F. Paoni
;  APPLICANT:  Margaret Ann Roy
;  APPLICANT:  Timothy A. Stewart
;  APPLICANT:  Daniel Tumas
;  APPLICANT:  Colin K. Watanabe
;  APPLICANT:  P.Mickey Williams
;  APPLICANT:  William I. Wood
;  APPLICANT:  Zemin Zang
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3130R1C7
;  CURRENT APPLICATION NUMBER: US/10/066,500
;  CURRENT FILING DATE:  2002-02-01
;  PRIOR APPLICATION NUMBER: 10/002,796
;  PRIOR FILING DATE: 2001-11-15
;  PRIOR APPLICATION NUMBER: 60/056974
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Query Match 100.0%; Score 609; DB 13; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-58;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
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; Publication No. US20030032057A1
; GENERAL INFORMATION:
; APPLICANT: Avi J. Ashkenazi
; APPLICANT: Kevin P. Baker
; APPLICANT: David A. Botstein
; APPLICANT: Luc Desnoyers
; APPLICANT: Dan L. Eaton
; APPLICANT: Napoleone Ferrara
; APPLICANT: Sherman Fong
; APPLICANT: Wei-Qiang Gao
; APPLICANT: Hanspeter Gerber
; APPLICANT: Mary E. Gerritsen
; APPLICANT: Audrey Goddard
; APPLICANT: Paul J. Godowski
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; APPLICANT: Ivar J. Kljavin
; APPLICANT: Jennie P. Mather
; APPLICANT: Mary A. Napier
; APPLICANT: James Pan
; APPLICANT: Nicholas F. Paoni
; APPLICANT: Margaret Ann Roy
; APPLICANT: Timothy A. Stewart
; APPLICANT: Daniel Tumas
; APPLICANT: Colin K. Watanabe
; APPLICANT: P.Mickey Williams
; APPLICANT: William I. Wood
; APPLICANT: Zemin Zang
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
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Query Match 100.0%; Score 609; DB 14; Length 117;
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; APPLICANT: Kevin P. Baker
; APPLICANT: David A. Botstein
; APPLICANT: Luc Desnoyers
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; APPLICANT: P.Mickey Williams
; APPLICANT: William I. Wood
; APPLICANT: Zemin Zang
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
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; PRIOR FILING DATE: 1998-09-16
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; PRIOR FILING DATE: 1998-11-25
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; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: PCT/US99/20111
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547

Query Match 100.0%; Score 609; DB 14; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-58;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQ 60

Qy         61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDK 117
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RESULT 6

US-10-066-494-9
; Sequence 9, Application US/10066494
; Publication No. US20030032063A1
; GENERAL INFORMATION:
; APPLICANT: Avi J. Ashkenazi
; APPLICANT: Kevin P. Baker
; APPLICANT: David A. Botstein
; APPLICANT: Luc Desnoyers
; APPLICANT: Dan L. Eaton
; APPLICANT: Napoleone Ferrara
; APPLICANT: Sherman Fong
; APPLICANT: Wei-Qiang Gao
; APPLICANT: Hanspeter Gerber
; APPLICANT: Mary E. Gerritsen
; APPLICANT: Audrey Goddard
; APPLICANT: Paul J. Godowski
; APPLICANT: Austin L. Gurney
; APPLICANT: Ivar J. Kljavin
; APPLICANT: Jennie P. Mather
; APPLICANT: Mary A. Napier
; APPLICANT: James Pan
; APPLICANT: Nicholas F. Paoni
; APPLICANT: Margaret Ann Roy
; APPLICANT: Timothy A. Stewart
; APPLICANT: Daniel Tumas
; APPLICANT: Colin K. Watanabe
; APPLICANT: P.Mickey Williams
; APPLICANT: William I. Wood
; APPLICANT: Zemin Zang
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3130R1C9
; CURRENT APPLICATION NUMBER: US/10/066,494
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 10/002,796
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059115
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; PRIOR APPLICATION NUMBER: PCT/US99/20111
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547

Query Match 100.0%; Score 609; DB 14; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-58;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDK 117
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Db         61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDK 117
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RESULT 7
US-10-066-269-9
; Sequence 9, Application US/10066269
; Publication No. US20030040014A1

; GENERAL INFORMATION:
; APPLICANT: Avi J. Ashkenazi
; APPLICANT: Kevin P. Baker
; APPLICANT: David A. Botstein
; APPLICANT: Luc Desnoyers
; APPLICANT: Dan L. Eaton
; APPLICANT: Napoleone Ferrara
; APPLICANT: Sherman Fong
; APPLICANT: Wei-Qiang Gao
; APPLICANT: Hanspeter Gerber
; APPLICANT: Mary E. Gerritsen
; APPLICANT: Audrey Goddard
; APPLICANT: Paul J. Godowski
; APPLICANT: Austin L. Gurney
; APPLICANT: Ivar J. Kljavin
; APPLICANT: Jennie P. Mather
; APPLICANT: Mary A. Napier
; APPLICANT: James Pan
; APPLICANT: Nicholas F. Paoni
; APPLICANT: Margaret Ann Roy
; APPLICANT: Timothy A. Stewart
; APPLICANT: Daniel Tumas
; APPLICANT: Colin K. Watanabe
; APPLICANT: P.Mickey Williams
; APPLICANT: William I. Wood
; APPLICANT: Zemin Zang
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3130R1C4
; CURRENT APPLICATION NUMBER: US/10/066,269
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 10/002,796
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/056974
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; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547

Query Match 100.0%; Score 609; DB 14; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-58;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db         61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDK 117
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RESULT 8
US-10-006-856A-6
; Sequence 6, Application US/10006856A
; Publication No. US20030044841A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C14
; CURRENT APPLICATION NUMBER: US/10/006,856A
; CURRENT FILING DATE: 2002-05-10
; NUMBER OF SEQ ID NOS: 477
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 6
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
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; NAME/KEY: sig_peptide
; LOCATION: 1-16
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 18-24, 32-38, 34-40, 35-41, 51-57
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; OTHER INFORMATION: Casein Kinase II Phosphorylation Site.
US-10-006-856A-6

Query Match 100.0%; Score 609; DB 14; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-58;
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Qy         61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDK 117
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Db         61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDK 117
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RESULT 9
US-10-066-211-9
; Sequence 9, Application US/10066211
; Publication No. US20030044844A1
; GENERAL INFORMATION:
; APPLICANT: Avi J. Ashkenazi
; APPLICANT: Kevin P. Baker
; APPLICANT: David A. Botstein
; APPLICANT: Luc Desnoyers
; APPLICANT: Dan L. Eaton
; APPLICANT: Napoleone Ferrara
; APPLICANT: Sherman Fong
; APPLICANT: Wei-Qiang Gao
; APPLICANT: Hanspeter Gerber
; APPLICANT: Mary E. Gerritsen
; APPLICANT: Audrey Goddard
; APPLICANT: Paul J. Godowski
; APPLICANT: Austin L. Gurney
; APPLICANT: Ivar J. Kljavin
; APPLICANT: Jennie P. Mather
; APPLICANT: Mary A. Napier
; APPLICANT: James Pan
; APPLICANT: Nicholas F. Paoni

; APPLICANT: Margaret Ann Roy
; APPLICANT: Timothy A. Stewart
; APPLICANT: Daniel Tumas
; APPLICANT: Colin K. Watanabe
; APPLICANT: P.Mickey Williams
; APPLICANT: William I. Wood
; APPLICANT: Zemin Zang
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3130R1C8
; CURRENT APPLICATION NUMBER: US/10/066,211
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 10/002,796
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059115
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; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
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; PRIOR FILING DATE: 1997-12-16
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; PRIOR FILING DATE: 2001-05-25

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; PRIOR FILING DATE: 2001-05-30
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; PRIOR APPLICATION NUMBER: PCT/US98/14552
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; PRIOR APPLICATION NUMBER: PCT/US98/18824
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; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: PCT/US98/19437
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; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: PCT/US99/05028
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: PCT/US99/20111
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547

Query Match 100.0%; Score 609; DB 14; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-58;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQ 60
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Db          1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQ 60

Qy         61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDK 117
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Db         61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDK 117
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RESULT 10
US-10-066-193-9
; Sequence 9, Application US/10066193
; Publication No. US20030044902A1
; GENERAL INFORMATION:
; APPLICANT: Avi J. Ashkenazi
; APPLICANT: Kevin P. Baker
; APPLICANT: David A. Botstein
; APPLICANT: Luc Desnoyers
; APPLICANT: Dan L. Eaton
; APPLICANT: Napoleone Ferrara
; APPLICANT: Sherman Fong
; APPLICANT: Wei-Qiang Gao
; APPLICANT: Hanspeter Gerber
; APPLICANT: Mary E. Gerritsen
; APPLICANT: Audrey Goddard
; APPLICANT: Paul J. Godowski
; APPLICANT: Austin L. Gurney
; APPLICANT: Ivar J. Kljavin
; APPLICANT: Jennie P. Mather
; APPLICANT: Mary A. Napier
; APPLICANT: James Pan
; APPLICANT: Nicholas F. Paoni
; APPLICANT: Margaret Ann Roy
; APPLICANT: Timothy A. Stewart
; APPLICANT: Daniel Tumas
; APPLICANT: Colin K. Watanabe
; APPLICANT: P.Mickey Williams
; APPLICANT: William I. Wood
; APPLICANT: Zemin Zang
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3130R1C3
; CURRENT APPLICATION NUMBER: US/10/066,193
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 10/002,796
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
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; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059588
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; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/062816
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063082
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/063329
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: 60/063733
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; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: PCT/US99/20111
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547

Query Match 100.0%; Score 609; DB 14; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-58;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQ 60

Qy         61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDK 117
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Db         61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDK 117
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RESULT 11
US-10-006-818A-6
; Sequence 6, Application US/10006818A
; Publication No. US20030054406A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan 1.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C4
; CURRENT APPLICATION NUMBER: US/10/006,818A
; CURRENT FILING DATE: 2001-12-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 6
; LENGTH: 117
; TYPE: PRT

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1-16
; OTHER INFORMATION: Signal Peptide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 18-24, 32-38, 34-40, 35-41, 51-57
; OTHER INFORMATION: N-Myristoylation Site.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 22-26, 50-54, 113-117
; OTHER INFORMATION: Casein Kinase II Phosphorylation Site.
US-10-006-818A-6

Query Match 100.0%; Score 609; DB 14; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-58;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQ 60
Db 1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQ 60

Qy 61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDK 117
Db 61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDK 117

RESULT 12
US-10-015-393A-6
; Sequence 6, Application US/10015393A
; Publication No. US20030069179A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C46
; CURRENT APPLICATION NUMBER: US/10/015,393A
; CURRENT FILING DATE: 2002-06-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 6
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1-16
; OTHER INFORMATION: Signal Peptide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 18-24, 32-38, 34-40, 35-41, 51-57
; OTHER INFORMATION: N-Myristoylation Site.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 22-26, 50-54, 113-117
; OTHER INFORMATION: Casein Kinase II Phosphorylation Site.
US-10-015-393A-6

Query Match 100.0%; Score 609; DB 14; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-58;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQ 60
Db 1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQ 60

Qy 61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDK 117
Db 61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDK 117

RESULT 13
US-10-015-869A-6
; Sequence 6, Application US/10015869A
; Publication No. US20030073130A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C45
; CURRENT APPLICATION NUMBER: US/10/015,869A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 6
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1-16
; OTHER INFORMATION: Signal Peptide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 18-24, 32-38, 34-40, 35-41, 51-57
; OTHER INFORMATION: N-Myristoylation Site.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 22-26, 50-54, 113-117
; OTHER INFORMATION: Casein Kinase II Phosphorylation Site.
US-10-015-869A-6

Query Match 100.0%; Score 609; DB 14; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-58;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQ 60
Db 1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQ 60

Qy 61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDK 117
Db 61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDK 117

RESULT 14
US-10-012-121A-6
; Sequence 6, Application US/10012121A
; Publication No. US20030073810A1

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; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C20
;  CURRENT APPLICATION NUMBER: US/10/012,121A
;  CURRENT FILING DATE:  2001-12-07
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 6
;   LENGTH: 117
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: sig_peptide
;   LOCATION: 1-16
;   OTHER INFORMATION: Signal Peptide
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 18-24, 32-38, 34-40, 35-41, 51-57
;   OTHER INFORMATION: N-Myristoylation Site.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 22-26, 50-54, 113-117
;   OTHER INFORMATION: Casein Kinase II Phosphorylation Site.
US-10-012-121A-6

  Query Match           100.0%;  Score 609;  DB 14;  Length 117;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-58;
  Matches  117;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQ 60
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Db          1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQ 60

Qy         61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDK 117
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Db         61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDK 117


RESULT 15
US-10-006-116A-6
; Sequence 6, Application US/10006116A
; Publication No. US20030082626A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C15
;  CURRENT APPLICATION NUMBER: US/10/006,116A
;  CURRENT FILING DATE:  2001-12-16
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;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098723
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;  PRIOR APPLICATION NUMBER: 60/098749
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; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28

Query Match 100.0%; Score 609; DB 14; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-58;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQ 60

Qy         61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDK 117
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDK 117
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Search completed: April 2, 2004, 09:56:13
Job time : 41 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 2, 2004, 09:37:06 ; Search time 39 Seconds
(without alignments)
946.555 Million cell updates/sec

Title: US-10-066-500-9
Perfect score: 609
Sequence: 1 MIVFGWAVFLASRSLGQGLL.....QNVDGLVLDTLAVIRTLVDK 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	604	99.2	576	4	Q96DX4	Q96dx4 homo sapien
2	586	96.2	576	6	Q95LP3	Q95lp3 macaca fasc
3	561	92.1	117	11	Q8BLS8	Q8bls8 mus musculu
4	556	91.3	576	11	Q8C039	Q8c039 mus musculu
5	556	91.3	576	11	Q8BVR6	Q8bvr6 mus musculu
6	86	14.1	601	16	Q82FI7	Q82fi7 streptomyce
7	85.5	14.0	290	5	Q20394	Q20394 caenorhabdi
8	79.5	13.1	356	10	Q9ATR4	Q9atr4 oryza sativ
9	79.5	13.1	388	10	Q941M8	Q941m8 oryza sativ
10	79.5	13.1	388	10	Q8LN68	Q8ln68 oryza sativ
11	79.5	13.1	388	10	Q7Y1X7	Q7y1x7 oryza sativ
12	79.5	13.1	5146	5	Q9VXR3	Q9vxr3 drosophila
13	79	13.0	970	10	Q9AYF2	Q9ayf2 oryza sativ
14	79	13.0	970	10	Q7XF23	Q7xf23 oryza sativ
15	78.5	12.9	188	2	Q7WX07	Q7wx07 alcaligenes
16	78	12.8	179	5	Q9XZ40	Q9xz40 plasmodium
17	78	12.8	191	5	Q9U0C1	Q9u0c1 plasmodium
18	78	12.8	203	5	Q9U0C0	Q9u0c0 plasmodium
19	78	12.8	480	5	Q27033	Q27033 theileria p
20	77.5	12.7	550	12	O40912	O40912 kaposi's sa
21	77.5	12.7	550	12	P88903	P88903 kaposi's sa
22	76.5	12.6	634	4	Q8IXW0	Q8ixw0 homo sapien
23	76	12.5	1063	16	Q8XXH5	Q8xxh5 ralstonia s
24	75.5	12.4	948	5	Q9U304	Q9u304 caenorhabdi
25	75	12.3	147	5	O15805	O15805 plasmodium
26	75	12.3	183	5	Q9U0B5	Q9u0b5 plasmodium
27	75	12.3	183	5	Q9U0B6	Q9u0b6 plasmodium
28	75	12.3	204	5	Q9U0B4	Q9u0b4 plasmodium
29	75	12.3	260	5	Q8IT83	Q8it83 plasmodium
30	75	12.3	267	13	Q9PUV0	Q9puv0 balistes sp
31	75	12.3	278	5	Q25862	Q25862 plasmodium
32	75	12.3	291	5	Q25789	Q25789 plasmodium
33	74.5	12.2	121	12	Q8QRK4	Q8qrk4 hepatitis c
34	74.5	12.2	462	3	O42721	O42721 penicillium
35	74.5	12.2	2120	5	Q8IAK1	Q8iak1 plasmodium
36	74	12.2	850	16	Q8FML9	Q8fml9 corynebacte
37	73.5	12.1	416	12	Q81265	Q81265 hepatitis c
38	73	12.0	206	5	Q9U0C3	Q9u0c3 plasmodium
39	73	12.0	220	5	Q9U0B3	Q9u0b3 plasmodium
40	73	12.0	222	5	Q9U0B1	Q9u0b1 plasmodium
41	73	12.0	353	11	Q62313	Q62313 mus musculu
42	73	12.0	579	2	Q8GFF2	Q8gff2 streptomyce
43	73	12.0	1160	5	Q8T0V9	Q8t0v9 drosophila
44	73	12.0	1163	4	Q8N6U4	Q8n6u4 homo sapien
45	73	12.0	3571	10	Q9SL27	Q9sl27 arabidopsis

ALIGNMENTS

RESULT 1
Q96DX4
ID Q96DX4 PRELIMINARY; PRT; 576 AA.
AC Q96DX4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein KIAA1972.
GN KIAA1972.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=21842142; PubMed=11853319;
RA Nagase T., Kikuno R., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XXII.
RT The complete sequences of 50 new cDNA clones which code for large
RT proteins.";
RL DNA Res. 8:319-327(2001).
DR EMBL; BC013173; AAH13173.1; -.
DR EMBL; AB075852; BAB85558.1; -.
DR InterPro; IPR008938; ARM.
DR InterPro; IPR003877; SPRY_receptor.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00622; SPRY; 1.
DR SMART; SM00184; RING; 1.
DR SMART; SM00449; SPRY; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 576 AA; 64180 MW; 8598E43E96691F9B CRC64;

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  Query Match             99.2%;  Score 604;  DB 4;  Length 576;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-57;
  Matches  116;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQ 60
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Db          1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQ 60

Qy         61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVD 116
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Db         61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVD 116


RESULT 2
Q95LP3
ID   Q95LP3      PRELIMINARY;      PRT;   576 AA.
AC   Q95LP3;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
RA   Hashimoto K., Osada N., Hida M., Kusuda J., Tanuma R., Hirai M.,
RA   Terao K., Sugano S.;
RT   "Isolation of novel full-length cDNA clones from macaque testis cDNA
RT   libraries.";
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB072745; BAB69714.1; -.
DR   InterPro; IPR008938; ARM.
DR   InterPro; IPR003877; SPRY_receptor.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00622; SPRY; 1.
DR   SMART; SM00184; RING; 1.
DR   SMART; SM00449; SPRY; 1.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   576 AA;  64259 MW;  68D230AD1C4F5F8D CRC64;

  Query Match             96.2%;  Score 586;  DB 6;  Length 576;
  Best Local Similarity   97.4%;  Pred. No. 1.1e-55;
  Matches  113;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQ 60
              ||| |||||||||||||||||||||||||| || ||||||||||||||||||||||||||
Db          1 MIVLGWAVFLASRSLGQGLLLTLEEHIAHFLGTRGATTTMGNSCICRDDSGTDDSVDTQQ 60

Qy         61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVD 116
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVD 116


RESULT 3
Q8BLS8
ID   Q8BLS8      PRELIMINARY;      PRT;   117 AA.
AC   Q8BLS8;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical SPla and the RYanodine receptor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Cortex;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK043522; BAC31566.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   117 AA;  12738 MW;  D3FEC471ABD55D3C CRC64;

  Query Match             92.1%;  Score 561;  DB 11;  Length 117;
  Best Local Similarity   91.5%;  Pred. No. 9.5e-54;
  Matches  107;  Conservative    3;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQ 60
              |||||||||||||||||||||||||| ||| ||  |||||||||||| :|:||| |
Db          1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHLLGTTGATATMGNSCICRDDSGAEDNVDTHQ 60

Qy         61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDK 117
              ||||| |||||:||||||||||||||||||||||||||||||||||||||||||||
Db         61 QQAENSTVPTADSRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDK 117


RESULT 4
Q8C039
ID   Q8C039      PRELIMINARY;      PRT;   576 AA.
AC   Q8C039;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical SPla and the RYanodine receptor.
GN   4930470D19RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK032416; BAC27858.1; -.
DR   MGD; MGI:1914860; 4930470D19Rik.
DR   InterPro; IPR008938; ARM.
DR   InterPro; IPR003877; SPRY_receptor.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00622; SPRY; 1.
DR   SMART; SM00184; RING; 1.
DR   SMART; SM00449; SPRY; 1.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   576 AA;  64340 MW;  D72D60E803911D02 CRC64;

  Query Match             91.3%;  Score 556;  DB 11;  Length 576;
  Best Local Similarity   91.4%;  Pred. No. 2.2e-52;
  Matches  106;  Conservative    3;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQ 60
              |||||||||||||||||||||||||| ||| ||  |||||||||||| :|:||| |
Db          1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHLLGTTGATATMGNSCICRDDSGAEDNVDTHQ 60

Qy         61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVD 116
              ||||||||||:|||||||||||||||||||||||||||||||||||||||||||
Db         61 QQAENSTVPTADSRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVD 116


RESULT 5
Q8BVR6
ID   Q8BVR6      PRELIMINARY;      PRT;   576 AA.
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AC   Q8BVR6;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical SPla and the RYanodine receptor (Hypothetical
DE   protein).
GN   4930470D19RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RA   Strausberg R.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK076799; BAC36485.1; -.
DR   EMBL; BC054121; AAH54121.1; -.
DR   MGD; MGI:1914860; 4930470D19Rik.
DR   InterPro; IPR008938; ARM.
DR   InterPro; IPR003877; SPRY_receptor.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00622; SPRY; 1.
DR   SMART; SM00184; RING; 1.
DR   SMART; SM00449; SPRY; 1.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   576 AA;  64322 MW;  823C3532FCE18387 CRC64;

  Query Match           91.3%;  Score 556;  DB 11;  Length 576;
  Best Local Similarity  91.4%;  Pred. No. 2.2e-52;
  Matches  106;  Conservative    3;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQ 60
              ||||||||||||||||||||||||||||||| ||| ||  |||||||||||||| :|:||| |
Db          1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHLLGTTGATATMGNSCICRDDSGAEDNVDTHQ 60

Qy         61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVD 116
              |||||| |||||:|||||||||||||||||||||||||||||||||||||||||||||
Db         61 QQAENSTVPTADSRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVD 116
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RESULT 6
Q82FI7
ID   Q82FI7      PRELIMINARY;      PRT;   601 AA.
AC   Q82FI7;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Putative thiamine biosynthesis protein.
GN   THIA OR SAV4265.
OS   Streptomyces avermitilis.
OC   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC   Streptomycineae; Streptomycetaceae; Streptomyces.
OX   NCBI_TaxID=33903;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX   MEDLINE=21477403; PubMed=11572948;
RA   Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA   Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
RA   Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT   "Genome sequence of an industrial microorganism Streptomyces
RT   avermitilis: deducing the ability of producing secondary
RT   metabolites.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX   MEDLINE=22608306; PubMed=12692562;
RA   Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA   Sakaki Y., Hattori M., Omura S.;
RT   "Complete genome sequence and comparative analysis of the industrial
RT   microorganism Streptomyces avermitilis.";
RL   Nat. Biotechnol. 21:526-531(2003).
DR   EMBL; AP005038; BAC71977.1; -.
DR   GO; GO:0009228; P:thiamin biosynthesis; IEA.
DR   InterPro; IPR002817; ThiC.
DR   Pfam; PF01964; ThiC; 1.
DR   ProDom; PD007048; ThiC; 1.
DR   TIGRFAMs; TIGR00190; thiC; 1.
KW   Complete proteome.
SQ   SEQUENCE   601 AA;  66485 MW;  B149CD75A602FCF5 CRC64;

  Query Match           14.1%;  Score 86;  DB 16;  Length 601;
  Best Local Similarity  32.3%;  Pred. No. 0.86;
  Matches   31;  Conservative    7;  Mismatches   36;  Indels   22;  Gaps    4;

Qy         39 TMGNSCICRDDSG--TDDSVDTQQQQA-----ENSAVPTADTRSQPRDPVRP-------- 83
              | | |     | ||  || |||| ::       ||  :   ||       ||||
Db         55 TNGESVTLYDTSGPYTDPSVDTDVRRGLAPLRENWIIARGDTEEYAGRPVRPEDDGIKHT 114

Qy         84 -PRRGRG------PHEPRRKKQNVDGLVLDTLAVIR 112
              || |         |  ||: ::  ||  :  ||  |
Db        115 SPRGGLRNLDAVFPGRPRQPRRGRDGQAVTQLAYAR 150


RESULT 7
Q20394
ID   Q20394      PRELIMINARY;      PRT;   290 AA.
AC   Q20394;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   F44D12.6 protein.
GN   F44D12.6.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Coles L.;
```

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RL   Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99069613; PubMed=9851916;
RA   none;
RT   "Genome sequence of the nematode C.elegans: A platform for
RT   investigating biology.";
RL   Science 282:2012-2018(1998).
DR   EMBL; Z68298; CAA92602.1; -.
DR   PIR; T22161; T22161.
DR   WormPep; F44D12.6; CE03330.
SQ   SEQUENCE   290 AA;  32831 MW;  B60BEFE9C89E7780 CRC64;

  Query Match             14.0%;  Score 85.5;  DB 5;  Length 290;
  Best Local Similarity   30.0%;  Pred. No. 0.42;
  Matches   27;  Conservative   15;  Mismatches   31;  Indels   17;  Gaps    5;

Qy         24 EEHIAHFLGTGGAATTMGN-SCICRDDSGTD-----DSVDTQQQQAENSAVPTADTRSQP 77
              : |: |:  || |     | :|  :|| | |     :| : |::   || :| :|
Db        154 DAHV-HWRETGLAFIIRSNDACRSKDDGGCDTIDSQNSKEDQERSKVNSEMPLSD----- 207

Qy         78 RDPVRPPRRGRGPHEPRRKKQNVDGLVLDT 107
              : | | |:       ||| ||   | :: |
Db        208 KKPDRKPQ-----ETPRRSKQRTPGPMMPT 232


RESULT 8
Q9ATR4
ID   Q9ATR4      PRELIMINARY;      PRT;   356 AA.
AC   Q9ATR4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Teosinte branched1 protein (Fragment).
GN   TB1.
OS   Oryza sativa (Rice).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=4530;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21165336; PubMed=11264415;
RA   Lukens L., Doebley J.;
RT   "Molecular evolution of the teosinte branched gene among maize and
RT   related rrasses.";
RL   Mol. Biol. Evol. 18:627-638(2001).
DR   EMBL; AF322143; AAK37505.1; -.
DR   Gramene; Q9ATR4; -.
DR   InterPro; IPR005333; TCP.
DR   Pfam; PF03634; TCP; 1.
FT   NON_TER       1       1
FT   NON_TER     356     356
SQ   SEQUENCE   356 AA;  37757 MW;  95D7174BC6AB8F84 CRC64;

  Query Match             13.1%;  Score 79.5;  DB 10;  Length 356;
  Best Local Similarity   32.3%;  Pred. No. 2.4;
  Matches   20;  Conservative    6;  Mismatches   27;  Indels    9;  Gaps    1;

Qy         43 SCICRDDSGTDDSVDTQQQQAENSA---------VPTADTRSQPRDPVRPPRRGRGPHEP 93
              | :| :|  :  ||| :|||  | |           |   |  : | :| |    | |
Db        180 SSVCEEDGSSSLSVDGKQQQHSNPADRGGGAGDHKGAAHGHSDGKKPAKPRRAAANPKPP 239

Qy         94 RR 95
              ||
Db        240 RR 241


RESULT 9
Q941M8
ID   Q941M8      PRELIMINARY;      PRT;   388 AA.
AC   Q941M8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Teosinte branched1 protein.
GN   TB1.
OS   Oryza sativa (Rice).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=4530;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. indica guanglu'ai 4;
RA   Hu W., Zhao Y., Luo D.;
RT   "The structural and functional analysis of a Tb1-like gene in rice.";
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY043215; AAL05595.1; -.
DR   Gramene; Q941M8; -.
DR   InterPro; IPR005333; TCP.
DR   Pfam; PF03634; TCP; 1.
SQ   SEQUENCE   388 AA;  41493 MW;  700E90C018BC66A0 CRC64;

  Query Match             13.1%;  Score 79.5;  DB 10;  Length 388;
  Best Local Similarity   32.3%;  Pred. No. 2.7;
  Matches   20;  Conservative    6;  Mismatches   27;  Indels    9;  Gaps    1;

Qy         43 SCICRDDSGTDDSVDTQQQQAENSA---------VPTADTRSQPRDPVRPPRRGRGPHEP 93
              | :| :|  :  ||| :|||  | |           |   |  : | :| |    | |
Db        179 SSVCEEDGSSSLSVDGKQQQHSNPADRGGGAGDHKGAAHGHSDGKKPAKPRRAAANPKPP 238

Qy         94 RR 95
              ||
Db        239 RR 240


RESULT 10
Q8LN68
ID   Q8LN68      PRELIMINARY;      PRT;   388 AA.
AC   Q8LN68;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Teosinte branched1 protein.
GN   OSJNBA0004G17.5 OR OSTB1.
OS   Oryza sativa (japonica cultivar-group).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=39947;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Nipponbare;
RA   Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
RA   Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
RA   Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
RA   Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
RA   Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
RA   White O., Salzberg S.L., Fraser C.M.;
RT   "Oryza sativa chromosome 3 BAC OSJNBa0004G17 genomic sequence.";
RL   Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Nipponbare;
RA   Takeda T., Suwa Y., Ueguchi-Tanaka M., Ashikari M., Matsuoka M.,
RA   Ueguchi C.;
RT   "The OsTB1 gene negatively regulates lateral branching in rice.";
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC091775; AAM97162.1; -.
DR   EMBL; AB088343; BAC54954.1; -.
DR   Gramene; Q8LN68; -.
DR   InterPro; IPR005333; TCP.
DR   Pfam; PF03634; TCP; 1.
SQ   SEQUENCE   388 AA;  41504 MW;  8CF363D2EAA02743 CRC64;
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  Query Match             13.1%;  Score 79.5;  DB 10;  Length 388;
  Best Local Similarity   32.3%;  Pred. No. 2.7;
  Matches   20;  Conservative    6;  Mismatches   27;  Indels    9;  Gaps    1;

Qy         43 SCICRDDSGTDDSVDTQQQQAENSA---------VPTADTRSQPRDPVRPPRRGRGPHEP 93
              | :| :|  :  ||| :|||  | |             |   |  : | :| |    | |
Db        179 SSVCEEDGSSSLSVDGKQQQHSNPADRGGGAGDHKGAAHGHSDGKKPAKPRRAAANPKPP 238

Qy         94 RR 95
              ||
Db        239 RR 240


RESULT 11
Q7Y1X7
ID   Q7Y1X7      PRELIMINARY;      PRT;   388 AA.
AC   Q7Y1X7;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Teosinte-branching 1.
GN   TB1.
OS   Oryza sativa (indica cultivar-group).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=39946;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. IR-36;
RA   Hu W., Zhang S., Zhao Z., Zhao Y., Sun C.R., Luo D.;
RT   "The structural and expression analysis of OsTB1 in rice.";
RL   Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY286002; AAP37176.1; -.
SQ   SEQUENCE   388 AA;  41504 MW;  8CF363D2EAA02743 CRC64;

  Query Match             13.1%;  Score 79.5;  DB 10;  Length 388;
  Best Local Similarity   32.3%;  Pred. No. 2.7;
  Matches   20;  Conservative    6;  Mismatches   27;  Indels    9;  Gaps    1;

Qy         43 SCICRDDSGTDDSVDTQQQQAENSA---------VPTADTRSQPRDPVRPPRRGRGPHEP 93
              | :| :|  :  ||| :|||  | |             |   |  : | :| |    | |
Db        179 SSVCEEDGSSSLSVDGKQQQHSNPADRGGGAGDHKGAAHGHSDGKKPAKPRRAAANPKPP 238

Qy         94 RR 95
              ||
Db        239 RR 240


RESULT 12
Q9VXR3
ID   Q9VXR3      PRELIMINARY;      PRT;  5146 AA.
AC   Q9VXR3;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   CG8184 protein.
GN   CG8184.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Berkeley;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
RA   Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA   Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
RA   Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA   Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA   Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA   Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA   Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA   McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA   Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA   Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA   Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
RA   Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT   "Sequencing of Drosophila melanogaster genome.";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA   Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
RA   Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
RA   Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA   Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA   Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA   Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT   "Annotation of Drosophila melanogaster genome.";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RA   FlyBase;
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AE003500; AAF48495.2; -.
DR   FlyBase; FBgn0030674; CG8184.
DR   GO; GO:0005622; C:intracellular; IEA.
DR   GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR   GO; GO:0005488; F:binding; IEA.
```

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DR   GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   GO; GO:0006512; P:ubiquitin cycle; IEA.
DR   InterPro; IPR008938; ARM.
DR   InterPro; IPR000569; HECT_domain.
DR   InterPro; IPR001993; Mitoch_carrier.
DR   InterPro; IPR000449; UBA_domain.
DR   InterPro; IPR004170; WWE_dom.
DR   Pfam; PF00632; HECT; 1.
DR   Pfam; PF00627; UBA; 1.
DR   Pfam; PF02825; WWE; 1.
DR   SMART; SM00119; HECTc; 1.
DR   PROSITE; PS50237; HECT; 1.
DR   PROSITE; PS00215; MITOCH_CARRIER; 1.
DR   PROSITE; PS50030; UBA; 1.
SQ   SEQUENCE   5146 AA;  556847 MW;  27BF187F2D279846 CRC64;

  Query Match             13.1%;  Score 79.5;  DB 5;  Length 5146;
  Best Local Similarity   30.1%;  Pred. No. 54;
  Matches   22;  Conservative    8;  Mismatches   30;  Indels   13;  Gaps    2;

Qy         32 GTGGAATTMGNSCICRDDSGTDDSVDTQQQQAENSAVPTADTRSQPRDPVRPPRRGRGPH 91
              ||| |:: :  :    | || ||  | :   |           || :       | :| ||
Db        853 GTGSASSVLQGAADTNDSSGDDDDDDDEMSSA----------SQQQQQPTTPGQGGGPS 901

Qy         92 EPRRKKQNVDGLV 104
              ||   |   |:|
Db        902 TPR--TQQAGGVV 912


RESULT 13
Q9AYF2
ID   Q9AYF2      PRELIMINARY;      PRT;   970 AA.
AC   Q9AYF2;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Similar to Zea mays chromosome 422kDazein-associated intercluster
DE   region,copia-typepolpolyprotein.
GN   OSJNBA0094J09.18.
OS   Oryza sativa (Rice).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=4530;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   See L.H., Spiegel L.A., Nascimento L.U., de la Bastide M.,
RA   Preston R.R., Huange E.N., Rodriguez M.A., Vil M.D., Baker J.P.,
RA   Bahret A., Shah R.S., Miller B., Kirchoff K.A., King L., Toth K.,
RA   O'Shaughnessy A., Dedhia N.N., McCombie W.R.;
RT   "Genomic Sequence For Oryza sativa, Nipponbare strain, Chromosome X,
RT   Clone OSJNBa0094J09, complete sequence.";
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   McCombie W.R.;
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   McCombie W.R.;
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Bal H.P., See L.H., Spiegel L.A., Nascimento L.U., de la Bastide M.,
RA   Preston R.R., Huange E.N., Rodriguez M.A., Vil M.D., Baker J.P.,
RA   Bahret A., Shah R.S., Miller B., Kirchoff K.A., King L., Toth K.,
RA   O'Shaughnessy A., Dedhia N.N., McCombie W.R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC078839; AAK13102.1; -.
DR   Gramene; Q9AYF2; -.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0004289; F:subtilase activity; IEA.
DR   GO; GO:0006310; P:DNA recombination; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR000209; Peptidase_S8.
DR   InterPro; IPR001584; Rve.
DR   Pfam; PF00665; rve; 1.
DR   PROSITE; PS00136; SUBTILASE_ASP; 1.
SQ   SEQUENCE   970 AA;  108499 MW;  14D8F3EB056B194A CRC64;

  Query Match             13.0%;  Score 79;  DB 10;  Length 970;
  Best Local Similarity   27.4%;  Pred. No. 8.8;
  Matches   31;  Conservative   12;  Mismatches   42;  Indels   28;  Gaps    6;

Qy          4 FGWAVFLASRSLG----QGLLLTLEEHIAHFLGT--------GGAATTM--GNSCICRDD 49
              : |  |:|::        :|| | |:      | |:         ||  : :   :|||  ||
Db        551 YSWVFFMATKDEAFQHFRGLFLRLD---LEFPGSLKRIRSDNGGTLSQVQGEDSCIFEDD 607

Qy         50 SGTDDSVDTQQQQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDG 102
              |  ||         |    |  || |          ||  || | : |  :    |
Db        608 SDDDDDKVGSAGQTGRQAGQTAST---------PP--GRPPQDERSNRPGSSG 649


RESULT 14
Q7XF23
ID   Q7XF23      PRELIMINARY;      PRT;   970 AA.
AC   Q7XF23;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Similar to Zea mays chromosome 422kDazein-associated intercluster
DE   region,copia-typepolpolyprotein.
GN   OSJNBA0094J09.18.
OS   Oryza sativa (japonica cultivar-group).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=39947;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Nipponbare;
RA   The Rice Chromosome 10 Sequencing Consortium;
RT   "In-depth view of structure, activity, and evolution of rice
RT   chromosome 10.";
RL   Science 300:1566-1569(2003).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Nipponbare;
RA   Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AE017089; AAP53536.1; -.
KW   Polyprotein.
SQ   SEQUENCE   970 AA;  108499 MW;  14D8F3EB056B194A CRC64;

  Query Match             13.0%;  Score 79;  DB 10;  Length 970;
  Best Local Similarity   27.4%;  Pred. No. 8.8;
  Matches   31;  Conservative   12;  Mismatches   42;  Indels   28;  Gaps    6;

Qy          4 FGWAVFLASRSLG----QGLLLTLEEHIAHFLGT--------GGAATTM--GNSCICRDD 49
              : |  |:|::        :|| | |:      | |:         ||  : :   :|||  ||
Db        551 YSWVFFMATKDEAFQHFRGLFLRLD---LEFPGSLKRIRSDNGGTLSQVQGEDSCIFEDD 607

Qy         50 SGTDDSVDTQQQQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDG 102
              |  ||         |    |  || |          ||  || | : |  :    |
Db        608 SDDDDDKVGSAGQTGRQAGQTAST---------PP--GRPPQDERSNRPGSSG 649


RESULT 15
Q7WX07
ID   Q7WX07      PRELIMINARY;      PRT;   188 AA.
AC   Q7WX07;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Putative single-strand binding protein.
```

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GN   SSB OR PHG335.
OS   Alcaligenes eutrophus (Ralstonia eutropha).
OG   Plasmid megaplasmid pHG1.
OC   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC   Burkholderiaceae; Ralstonia.
OX   NCBI_TaxID=510;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=H16;
RA   Schwartz E., Henne A., Cramm R., Eitinger T., Friedrich B.,
RA   Gottschalk G.;
RT   "Complete Nucleotide Sequence of pHG1: A Ralstonia eutropha H16
RT   Megaplasmid Encoding Key Enzymes of H2-based Lithoautotropy and
RT   Anaerobiosis.";
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY305378; AAP86084.1; -.
KW   Plasmid.
SQ   SEQUENCE   188 AA;  20451 MW;  B43832FBCC232CF4 CRC64;

  Query Match             12.9%;  Score 78.5;  DB 2;  Length 188;
  Best Local Similarity   33.8%;  Pred. No. 1.5;
  Matches   26;  Conservative    8;  Mismatches   30;  Indels   13;  Gaps    5;

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Db        110 GRGGASD--GDS-----DSGTDRSASQQSPASAQRSAPTGQ-RQPPARRQPAQPPSNGFG 161

Qy         90 PHE---PRRKKQNVDGL 103
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Db        162 DFNEDIPFARPAALDGI 178


Search completed: April  2, 2004, 09:54:13
Job time : 42 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 2, 2004, 09:51:52 ; Search time 22 Seconds
(without alignments)
274.556 Million cell updates/sec

Title: US-10-066-500-9
Perfect score: 609
Sequence: 1 MIVFGWAVFLASRSLGQGLL.....QNVDGLVLDTLAVIRTLVDK 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	80	13.1	460	4	US-09-252-991A-20180	Sequence 20180, A
2	79	13.0	287	4	US-09-252-991A-30267	Sequence 30267, A
3	78	12.8	1527	4	US-09-418-710-27	Sequence 27, Appl
4	78	12.8	1531	4	US-09-418-710-29	Sequence 29, Appl
5	75	12.3	433	2	US-08-466-120-2	Sequence 2, Appli
6	75	12.3	433	5	PCT-US94-07266-2	Sequence 2, Appli
7	75	12.3	1525	4	US-09-418-710-69	Sequence 69, Appl
8	74.5	12.2	462	2	US-08-865-597A-2	Sequence 2, Appli
9	73.5	12.1	2509	2	US-08-149-097D-35	Sequence 35, Appl
10	73	12.0	623	3	US-09-029-348-3	Sequence 3, Appli
11	73	12.0	626	3	US-09-029-348-2	Sequence 2, Appli
12	72.5	11.9	333	4	US-09-252-991A-28443	Sequence 28443, A
13	71.5	11.7	562	4	US-09-252-991A-20178	Sequence 20178, A
14	71.5	11.7	566	4	US-09-252-991A-18531	Sequence 18531, A
15	71	11.7	863	4	US-09-252-991A-26099	Sequence 26099, A
16	70	11.5	396	4	US-09-252-991A-32927	Sequence 32927, A
17	69	11.3	191	2	US-08-290-665A-198	Sequence 198, App
18	69	11.3	191	2	US-08-290-665A-199	Sequence 199, App
19	69	11.3	191	2	US-08-290-665A-200	Sequence 200, App
20	69	11.3	191	2	US-08-290-665A-201	Sequence 201, App
21	69	11.3	191	2	US-08-290-665A-202	Sequence 202, App
22	69	11.3	191	2	US-08-290-665A-203	Sequence 203, App
23	69	11.3	191	5	PCT-US95-10398-198	Sequence 198, App
24	69	11.3	191	5	PCT-US95-10398-199	Sequence 199, App
25	69	11.3	191	5	PCT-US95-10398-200	Sequence 200, App
26	69	11.3	191	5	PCT-US95-10398-201	Sequence 201, App
27	69	11.3	191	5	PCT-US95-10398-202	Sequence 202, App
28	69	11.3	191	5	PCT-US95-10398-203	Sequence 203, App
29	69	11.3	319	4	US-08-635-886C-226	Sequence 226, App
30	69	11.3	319	4	US-08-974-690C-226	Sequence 226, App
31	69	11.3	350	4	US-09-252-991A-19537	Sequence 19537, A
32	69	11.3	498	4	US-09-354-151-2	Sequence 2, Appli
33	69	11.3	778	4	US-09-198-452A-508	Sequence 508, App
34	68.5	11.2	788	2	US-08-918-914-4	Sequence 4, Appli
35	68	11.2	149	4	US-09-252-991A-21599	Sequence 21599, A
36	68	11.2	379	4	US-09-252-991A-31693	Sequence 31693, A
37	68	11.2	882	3	US-09-413-814-78	Sequence 78, Appl
38	67.5	11.1	518	4	US-09-252-991A-18753	Sequence 18753, A
39	67.5	11.1	727	2	US-08-475-844-9	Sequence 9, Appli
40	67.5	11.1	727	5	PCT-US95-08429-9	Sequence 9, Appli
41	67.5	11.1	1298	2	US-08-690-473-2	Sequence 2, Appli
42	67.5	11.1	1298	3	US-09-259-821A-2	Sequence 2, Appli
43	67.5	11.1	1298	3	US-08-843-659-2	Sequence 2, Appli
44	67	11.0	393	4	US-09-432-470-2	Sequence 2, Appli
45	67	11.0	393	4	US-09-432-470-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-252-991A-20180
; Sequence 20180, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20180
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20180

Query Match 13.1%; Score 80; DB 4; Length 460;
Best Local Similarity 28.6%; Pred. No. 0.42;
Matches 20; Conservative 11; Mismatches 23; Indels 16; Gaps 2;

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Qy         32 GTGGAATTMGNSCICRDDSGTDDSVDTQQQQAENSAVPTADTRSQPRDPVRPPRRGRGPH 91
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Db        373 GQGQAAVQAG-----------EQADPEQRRVPGEAIQA----NRGEDPVEPPGERRGDH 416

Qy         92 EPRRKKQNVD 101
              | :|: ::||
Db        417 EQQRQGRHVD 426
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RESULT 2
US-09-252-991A-30267
; Sequence 30267, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30267
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30267

Query Match 13.0%; Score 79; DB 4; Length 287;
Best Local Similarity 37.5%; Pred. No. 0.3;
Matches 21; Conservative 7; Mismatches 24; Indels 4; Gaps 1;

Qy 51 GTDDSVDTQQQQAENSAVPTADTRSQPRDPVRPP----RRGRGPHEPRRKKQNVDG 102
Db 15 GRDPGKRTQQRRRDHPAGPVARARPGPARPRRRPGGLAGRGRGAGKHRRRPRQVPG 70

RESULT 3
US-09-418-710-27
; Sequence 27, Application US/09418710
; Patent No. 6596482
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-042001
; CURRENT APPLICATION NUMBER: US/09/418,710
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01783
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JP 9/310027
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: JP 9/116570
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 1527
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-418-710-27

Query Match 12.8%; Score 78; DB 4; Length 1527;
Best Local Similarity 27.5%; Pred. No. 3.5;
Matches 22; Conservative 12; Mismatches 26; Indels 20; Gaps 3;

Qy 48 DDSGTDDSVDTQQQQAENSAVPTADTRSQPRDPVR------PP------RRGRGPHEPRR 95
Db 1255 EDDESDEEEEEEEEEEEEDYEVAGLRLRPRKTIRGKHSVIPPAARSGRRPGKKPHSTRR 1314

Qy 96 KK--------QNVDGLVLDT 107
Db 1315 SQPKAPPVDDAEVDELVLQT 1334

RESULT 4
US-09-418-710-29
; Sequence 29, Application US/09418710
; Patent No. 6596482
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-042001
; CURRENT APPLICATION NUMBER: US/09/418,710
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01783
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JP 9/310027
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: JP 9/116570
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 1531
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-418-710-29

Query Match 12.8%; Score 78; DB 4; Length 1531;
Best Local Similarity 27.5%; Pred. No. 3.5;
Matches 22; Conservative 12; Mismatches 26; Indels 20; Gaps 3;

Qy 48 DDSGTDDSVDTQQQQAENSAVPTADTRSQPRDPVR------PP------RRGRGPHEPRR 95
Db 1259 EDDESDEEEEEEEEEEEEDYEVAGLRLRPRKTIRGKHSVIPPAARSGRRPGKKPHSTRR 1318

Qy 96 KK--------QNVDGLVLDT 107
Db 1319 SQPKAPPVDDAEVDELVLQT 1338

RESULT 5
US-08-466-120-2
; Sequence 2, Application US/08466120
; Patent No. 5869284
; GENERAL INFORMATION:
; APPLICANT: CAO, ET AL.
; TITLE OF INVENTION: Retinoic Acid Receptor Epsilon
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,120
; FILING DATE: June 6, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07266
; FILING DATE: 24 JUN 94
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-354
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 433 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-466-120-2

Query Match 12.3%; Score 75; DB 2; Length 433;
Best Local Similarity 35.0%; Pred. No. 1.5;
Matches 21; Conservative 12; Mismatches 23; Indels 4; Gaps 3;

Qy 35 GAATTMGNSCICRDDSGTDDSVDTQQQQAENSAVPTA-DTRSQ-PRDP--VRPPRRGRGP 90
Db 29 GSQAQGGSSCILREEARMPHSAGGTAGVGLEAAEPTALLTRAEPPSEPTEIRPPKRKKGP 88

RESULT 6
PCT-US94-07266-2
; Sequence 2, Application PC/TUS9407266

```
;  GENERAL INFORMATION:
;    APPLICANT:  CAO, ET AL.
;    TITLE OF INVENTION:  Retinoic Acid Receptor Epsilon
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/07266
;      FILING DATE:  Concurrently
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FERRARO, GREGORY D.
;      REGISTRATION NUMBER:  36,134
;      REFERENCE/DOCKET NUMBER:  325800-125
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  433 AMINO ACIDS
;      TYPE:  AMINO ACID
;      STRANDEDNESS:
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  PROTEIN
PCT-US94-07266-2

  Query Match             12.3%;  Score 75;  DB 5;  Length 433;
  Best Local Similarity   35.0%;  Pred. No. 1.5;
  Matches   21;  Conservative   12;  Mismatches   23;  Indels    4;  Gaps    3;

Qy         35 GAATTMGNSCICRDDSGTDDSVDTQQQQAENSAVPTA-DTRSQ-PRDP--VRPPRRGRGP 90
              |:    |:||| |:::    |          :| |||  ||:: | :|  :|||:| :||
Db         29 GSQAQGGSSCILREEARMPHSAGGTAGVGLEAAEPTALLTRAEPPSEPTEIRPPKRKKGP 88


RESULT 7
US-09-418-710-69
; Sequence 69, Application US/09418710
; Patent No. 6596482
; GENERAL INFORMATION:
;  APPLICANT:  Jones, Michael H.
;  TITLE OF INVENTION:  TRANSCRIPTIONAL REGULATOR
;  FILE REFERENCE:  06501-042001
;  CURRENT APPLICATION NUMBER: US/09/418,710
;  CURRENT FILING DATE:  1999-10-15
;  PRIOR APPLICATION NUMBER:  PCT/JP98/01783
;  PRIOR FILING DATE:  1998-04-17
;  PRIOR APPLICATION NUMBER:  JP 9/310027
;  PRIOR FILING DATE:  1997-10-24
;  PRIOR APPLICATION NUMBER:  JP 9/116570
;  PRIOR FILING DATE:  1997-04-18
;  NUMBER OF SEQ ID NOS:  73
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 69
;    LENGTH: 1525
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-418-710-69

  Query Match             12.3%;  Score 75;  DB 4;  Length 1525;
  Best Local Similarity   27.9%;  Pred. No. 7.9;
  Matches   24;  Conservative   12;  Mismatches   24;  Indels   26;  Gaps    4;

Qy         48 DDSGTDDSVD-------TQQQQAENSAVPTADTRSQPRDPVR------PP------RRGR 88
              ::| ::|| |         :::: |       |  | :||  :|       ||      | |:
Db       1246 EESASEDSEDESDEEEEEEEEEEEEDYEVAGLRLRPRKTIRGKHSVIPPAARSGRRPGK 1305

Qy         89 GPHEPRRKK-------QNVDGLVLDT 107
                 ||  || :          || ||| |
Db       1306 KPHSTRRSQPKAPPVDAEVDELVLQT 1331


RESULT 8
US-08-865-597A-2
; Sequence 2, Application US/08865597A
; Patent No. 5973131
;  GENERAL INFORMATION:
;    APPLICANT:  Cao, Liang
;    APPLICANT:  Yuen, Kwok Yung
;    TITLE OF INVENTION:  PENNICILLUM MARNEFFEI ANTIGENIC PROTEIN 1
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham LLP
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/865,597A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Chan, Albert Wai-Kit
;      REGISTRATION NUMBER:  36,479
;      REFERENCE/DOCKET NUMBER:  50288-A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 278-0400
;      TELEFAX:  (212) 391-0525
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  462 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-865-597A-2

  Query Match             12.2%;  Score 74.5;  DB 2;  Length 462;
  Best Local Similarity   29.2%;  Pred. No. 1.9;
  Matches   21;  Conservative   10;  Mismatches   36;  Indels    5;  Gaps    1;

Qy         12 SRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQQQAENSAVPTA 71
              || |  |:   ::: |  | ||| | ||          :: |  :  |  |  |:: ||
Db        328 SRQLSDGIAAGIKKGIDAFAGTGPAPTTSST-----PEASTAPAPSTPPQTPEDTLVPAT 382

Qy         72 DTRSQPRDPVRP 83
                | :    | |
Db        383 STPAPGPAPTAP 394


RESULT 9
US-08-149-097D-35
; Sequence 35, Application US/08149097D
; Patent No. 5874236
;  GENERAL INFORMATION:
;    APPLICANT:  Harpold, Michael
```

```
;    APPLICANT:  Ellis, Steven
;    APPLICANT:  Williams, Mark
;    APPLICANT:  Feldman, Daniel
;    APPLICANT:  McCue, Ann
;    APPLICANT:  Brenner, Robert
;    TITLE OF INVENTION:  HUMAN CALCIUM CHANNEL COMPOSITIONS AND
;    TITLE OF INVENTION:  METHODS
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Brown, Martin, Haller & McClain
;      STREET:  1660 Union Street
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92101-2926
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/149,097D
;      FILING DATE:  05-NOV-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/105,536
;      FILING DATE:  11-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US92/06903
;      FILING DATE:  14-AUG-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/914,231
;      FILING DATE:  13-JUL-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/868,354
;      FILING DATE:  10-APR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/745,206
;      FILING DATE:  15-AUG-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/620,250
;      FILING DATE:  30-NOV-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/482,384
;      FILING DATE:  20-FEB-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/603,751
;      FILING DATE:  04-APR-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US89/01408
;      FILING DATE:  04-APR-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/176,899
;      FILING DATE:  04-APR-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seidman, Stephanie L.
;      REGISTRATION NUMBER:  33,779
;      REFERENCE/DOCKET NUMBER:  6362-55038
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 238-0999
;      TELEFAX:  (619) 238-0062
;  INFORMATION FOR SEQ ID NO:  35:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2509 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  internal
;    ORIGINAL SOURCE:
;    FEATURE:
;      OTHER INFORMATION:  /product= "Alpha1A-1 subunit of
;      OTHER INFORMATION:  human calcium channel"
US-08-149-097D-35

  Query Match             12.1%;  Score 73.5;  DB 2;  Length 2509;
  Best Local Similarity   24.2%;  Pred. No. 23;
  Matches   31;  Conservative    9;  Mismatches   39;  Indels   49;  Gaps    4;

Qy         12 SRSLGQGLLLTLEEHIAHFLGTGG-----AATTMGNSC---------------------- 44
              |||  :|      ||:||  |:       | :| | |
Db       2251 SRSPSEG-----REHMAHRQGSSSVSGSPAPSTSGTSTPRRGRRQLPQTPSTPRPHVSYS 2305

Qy         45 -ICRDDSGTDDSVDTQQQQAENSAV---------------PTADTRSQPRDPVRPPRRG 87
               : |    |:        |||| :  ||              |||:  :  | ||     |
Db       2306 PVIRKAGGSGPPQQQQQQQQQQQAVARPGRAATSGPRRYPGPTAEPLAGDRPPTGGHSSG 2365

Qy         88 RGPHEPRR 95
              | |  ||
Db       2366 RSPRMERR 2373


RESULT 10
US-09-029-348-3
; Sequence 3, Application US/09029348
; Patent No. 6171827
; GENERAL INFORMATION:
;  APPLICANT: THE VICTORIA UNIVERSITY OF MANCHESTER
;  TITLE OF INVENTION: NOVEL PROCOLLAGENS
;  FILE REFERENCE: d087857PUS LISTING
;  CURRENT APPLICATION NUMBER: US/09/029,348
;  CURRENT FILING DATE: 1998-05-07
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 623
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: SEQUENCE
;   OTHER INFORMATION: DERIVED FROM cDNA OF PROCOLLAGENS
US-09-029-348-3

  Query Match             12.0%;  Score 73;  DB 3;  Length 623;
  Best Local Similarity   28.8%;  Pred. No. 4.2;
  Matches   30;  Conservative   10;  Mismatches   36;  Indels   28;  Gaps    7;

Qy         16 GQGLLLTLEEH---IAHFLGTGGAATTMGNS-------------CICRDDSGT---DDS 55
              |  ||| |      :|      | : :| |               |:|  |||:   ||
Db          8 GSWLLLALLHPTIILAQQEAVEGGCSHLGQSYADRDVWKPEPCQICVC--DSGSVLCDDI 65

Qy         56 V-DTQQQQAENSAVP----TADTRSQPRDPVRPPRRGRGPHEPR 94
              : | |:    | :|      |      |  | |||  |:||  |:
Db         66 ICDDQELDCPNPEIPFGECCAVCPQPPTAPTRPP-NGQGPQGPK 108


RESULT 11
US-09-029-348-2
; Sequence 2, Application US/09029348
; Patent No. 6171827
; GENERAL INFORMATION:
;  APPLICANT: THE VICTORIA UNIVERSITY OF MANCHESTER
;  TITLE OF INVENTION: NOVEL PROCOLLAGENS
;  FILE REFERENCE: d087857PUS LISTING
;  CURRENT APPLICATION NUMBER: US/09/029,348
;  CURRENT FILING DATE: 1998-05-07
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 626
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: SEQUENCE
```

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;   OTHER INFORMATION: DERIVED FROM cDNA OF PROCOLLAGENS
US-09-029-348-2

  Query Match             12.0%;  Score 73;  DB 3;  Length 626;
  Best Local Similarity   28.8%;  Pred. No. 4.2;
  Matches   30;  Conservative   10;  Mismatches   36;  Indels   28;  Gaps    7;

Qy         16 GQGLLLTLEEH---IAHFLGTGGAATTMGNS-------------CICRDDSGT---DDS 55
              |  ||| |       :|      |  : :| |             |:|  |||:    ||
Db          8 GSWLLLALLHPTIILAQQEAVEGGCSHLGQSYADRDVWKPEPCQICVC--DSGSVLCDDI 65

Qy         56 V-DTQQQQAENSAVP----TADTRSQPRDPVRPPRRGRGPHEPR 94
              : | |:     |  :|      |      |  | |||  |:||  |:
Db         66 ICDDQELDCPNPEIPFGECCAVCPQPPTAPTRPP-NGQGPQGPK 108


RESULT 12
US-09-252-991A-28443
; Sequence 28443, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 28443
;   LENGTH: 333
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28443

  Query Match             11.9%;  Score 72.5;  DB 4;  Length 333;
  Best Local Similarity   27.5%;  Pred. No. 2.1;
  Matches   25;  Conservative    7;  Mismatches   24;  Indels   35;  Gaps    3;

Qy         29 HFLGTGGAATTMGNSCICRDDSGTDDSVDTQQQQAENSAVP------TADTRSQPRDPVR 82
              | | |||             | | |:   | :|| :    |          | | :  :| |
Db        216 HRLRTGG-------------DEGADEGRHHQPRQAAHRRRPLPGPDRAGDHRRRGAEPDR 262

Qy         83 P---------------PRRGRGPHEPRRKK 97
                             ||| || | |||::
Db        263 QRTGDPAGHREAPGSLRPRRPRGHHLPRRRR 293


RESULT 13
US-09-252-991A-20178
; Sequence 20178, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 20178
;   LENGTH: 562
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20178

  Query Match             11.7%;  Score 71.5;  DB 4;  Length 562;
  Best Local Similarity   29.7%;  Pred. No. 5.5;
  Matches   22;  Conservative    6;  Mismatches   29;  Indels   17;  Gaps    2;

Qy         36 AATTMGNSCICRDDSGTDDSVDTQQQQAENSAVPTADTRSQPRDPVRPPRRGRGPHEP-- 93
              |||  |            :|      | :    | | :   :|| || || || || ||   |
Db         79 AATPAG-----------EDGGQLHQGRRPRLAGPGSGAGAQPADPRRPGRRRRGAQRPPP 127

Qy         94 ----RRKKQNVDGL 103
                  | ::   | |
Db        128 VAGSRARRSGTDAL 141


RESULT 14
US-09-252-991A-18531
; Sequence 18531, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 18531
;   LENGTH: 566
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18531

  Query Match             11.7%;  Score 71.5;  DB 4;  Length 566;
  Best Local Similarity   23.6%;  Pred. No. 5.6;
  Matches   29;  Conservative   10;  Mismatches   37;  Indels   47;  Gaps    4;

Qy         23 LEEHIAHFLGTGGAATTMGNSC--ICRDDSGTDDSVD---------TQQQQAENSAVPTA 71
              ||  :  | |  | ||     ||  | |   |  |||          |::    :    :
Db        118 LERRLRQFPGAQGTATGRRRSCQRIVRQAPGPGRSVDPPGHQGPPHAQRRAGSGTEGNAS 177

Qy         72 DTRSQPRDP-----------------------VRPPRR------------GRGPHEPRR 95
              ||  || |                      :|| ||                | |: | |
Db        178 RTRRAPRAPGQGQLPAGKRGQVRQAGDRGGARQLRPSRRPAAGTRLLHGPAARRPYRPAR 237

Qy         96 KKQ 98
              :::
Db        238 RQR 240


RESULT 15
US-09-252-991A-26099
; Sequence 26099, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 26099
;   LENGTH: 863
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26099
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Query Match 11.7%; Score 71; DB 4; Length 863;
Best Local Similarity 29.1%; Pred. No. 11;
Matches 25; Conservative 8; Mismatches 33; Indels 20; Gaps 3;

```
Qy         31 LGTGGAATT---------MGNSCICRDDSGTDDSVDTQQQQAENSAVPTADT------RS 75
              || | ||             |   : | |:|  | :    :::   | | |       |
Db        335 LGPGTAARRTHRPWPGRGAGGDALLRPDAGQADRLRGDPRRSPAQADPRAGALRAAGGRR 394

Qy         76 QPRDPVRPP-----RRGRGPHEPRRK 96
              ||  | :||     || || |   |:
Db        395 QPAVPRQPPGASGLRRRRGDHRLHRR 420
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Search completed: April 2, 2004, 09:55:20
Job time : 23 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 2, 2004, 09:35:21 ; Search time 17 Seconds
(without alignments)
358.365 Million cell updates/sec

Title: US-10-066-500-9
Perfect score: 609
Sequence: 1 MIVFGWAVFLASRSLGQGLL.....QNVDGLVLDTLAVIRTLVDK 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	79	13.0	612	1	THIC_STRCO	Q9x9u0 streptomyce
2	78.5	12.9	188	1	SSB_ALCEU	P59927 alcaligenes
3	78	12.8	1483	1	BA1B_HUMAN	Q9uig0 homo sapien
4	75	12.3	286	1	MSA2_PLAF1	P50496 plasmodium
5	73.5	12.1	2505	1	CCAA_HUMAN	O00555 homo sapien
6	73	12.0	281	1	MSA2_PLAFH	Q99319 plasmodium
7	73	12.0	353	1	TGN1_MOUSE	Q62313 mus musculu
8	73	12.0	1466	1	CA13_HUMAN	P02461 homo sapien
9	72.5	11.9	262	1	MSA2_PLAFC	Q99317 plasmodium
10	72.5	11.9	272	1	MSA2_PLAF7	P50498 plasmodium
11	72.5	11.9	274	1	MSA2_PLAF6	P50497 plasmodium
12	72.5	11.9	287	1	MSA2_PLAFG	P19260 plasmodium
13	72.5	11.9	300	1	MSA2_PLAFI	Q03644 plasmodium
14	72.5	11.9	300	1	MSA2_PLAFZ	Q03645 plasmodium
15	72.5	11.9	302	1	MSA2_PLAF9	Q03994 plasmodium
16	72.5	11.9	347	1	MSA2_PLAF2	Q03646 plasmodium
17	72.5	11.9	458	1	YNE1_CAEEL	P30640 caenorhabdi
18	72	11.8	1787	1	CHD3_CAEEL	Q22516 caenorhabdi
19	71	11.7	1479	1	BA1B_MOUSE	Q9z277 mus musculu
20	70.5	11.6	3726	1	TRX_DROME	P20659 drosophila
21	70	11.5	445	1	NRH3_MOUSE	Q9z0y9 mus musculu
22	69	11.3	1944	1	CHD3_HUMAN	Q12873 homo sapien
23	68	11.2	424	1	COT1_BOVIN	Q9ttr8 bos taurus
24	68	11.2	445	1	NRH3_RAT	Q62685 rattus norv
25	68	11.2	504	1	FTSY_SYNY3	P73930 synechocyst
26	68	11.2	702	1	EXO1_YEAST	P39875 saccharomyc
27	67.5	11.1	399	1	SIR3_HUMAN	Q9ntg7 homo sapien
28	67.5	11.1	727	1	CTCF_HUMAN	P49711 homo sapien
29	67.5	11.1	1298	1	ICP4_HSV11	P08392 herpes simp
30	67	11.0	393	1	CIW4_HUMAN	Q9nyg8 homo sapien
31	67	11.0	1202	1	NOS3_HUMAN	P29474 homo sapien
32	67	11.0	3828	1	TRX_DROVI	Q24742 drosophila
33	66.5	10.9	217	1	YKR4_EBV	P30117 epstein-bar
34	66.5	10.9	268	1	EP34_HCMVA	P16768 human cytom
35	66.5	10.9	276	1	MSA2_PLAF8	Q99320 plasmodium
36	66.5	10.9	343	1	GLN2_STRVR	P19432 streptomyce
37	66.5	10.9	423	1	COT1_HUMAN	P10589 homo sapien
38	66.5	10.9	684	1	EP84_HCMVA	P17151 human cytom
39	66	10.8	228	1	EFA5_HUMAN	P52803 homo sapien
40	66	10.8	228	1	EFA5_MOUSE	O08543 mus musculu
41	66	10.8	324	1	HE31_STRAW	Q82e76 streptomyce
42	66	10.8	736	1	DVL2_XENLA	P51142 xenopus lae
43	66	10.8	1021	1	MAPA_MOUSE	Q9qyr6 mus musculu
44	66	10.8	1380	1	CYAA_LEIDO	Q27675 leishmania
45	66	10.8	2716	1	OSA_DROME	Q8in94 drosophila

ALIGNMENTS

RESULT 1
THIC_STRCO
ID THIC_STRCO STANDARD; PRT; 612 AA.
AC Q9X9U0;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Thiamine biosynthesis protein thiC.
GN THIC OR SCO3928 OR SCQ11.11.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
RA Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
CC -!- FUNCTION: Required for the synthesis of the hydromethylpyrimidine
CC (HMP) moiety of thiamine (4-amino-2-methyl-5-
CC hydroxymethylpyrimidine) (By similarity).
CC -!- PATHWAY: Thiamine biosynthesis.
CC -!- SIMILARITY: Belongs to the thiC family.
CC ---
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CC ---
DR EMBL; AL939118; CAB46966.1; -.
DR PIR; T37181; T37181.
DR HAMAP; MF_00089; -; 1.
DR InterPro; IPR002817; ThiC.
DR Pfam; PF01964; ThiC; 1.
DR ProDom; PD007048; ThiC; 1.
DR TIGRFAMs; TIGR00190; thiC; 1.
KW Thiamine biosynthesis; Complete proteome.
SQ SEQUENCE 612 AA; 67371 MW; 290BF2454200CF68 CRC64;

Query Match 13.0%; Score 79; DB 1; Length 612;
Best Local Similarity 31.2%; Pred. No. 2.4;
Matches 30; Conservative 7; Mismatches 37; Indels 22; Gaps 4;

```
Qy          39 TMGNSCICRDDSG--TDDSVDTQQQQA-----ENSAVPTADTRSQPRDPVRP-------- 83
               | | |    | ||  ||  |||  ::      ||  :   ||       ||||
Db          60 TNGQSVTLYDTSGPYTDPLVDTDVRRGLAPLRENWIIARGDTEEYAGRPVRPEDDGIKHT 119

Qy          84 -PRRGRG------PHEPRRKKQNVDGLVLDTLAVIR 112
                || |         |  ||: ::  ||  :  ||  |
Db         120 SPRGGLRNLDAVFPGRPRQPRRGRDGNAVTQLAYAR 155


RESULT 2
SSB_ALCEU
ID   SSB_ALCEU      STANDARD;      PRT;   188 AA.
AC   P59927; Q7WX07;
DT   15-MAR-2004 (Rel. 43, Created)
DT   15-MAR-2004 (Rel. 43, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Single-strand binding protein (SSB) (Helix-destabilizing protein).
GN   SSB OR PHG335.
OS   Alcaligenes eutrophus (Ralstonia eutropha).
OG   Plasmid megaplasmid pHG1.
OC   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC   Burkholderiaceae; Ralstonia.
OX   NCBI_TaxID=510;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=H16 / DSM 428 / ATCC 17699;
RA   Schwartz E., Henne A., Cramm R., Eitinger T., Friedrich B.,
RA   Gottschalk G.;
RT   "Complete nucleotide sequence of pHG1: a Ralstonia eutropha H16
RT   megaplasmid encoding key enzymes of H2-based lithoautotropy and
RT   anaerobiosis.";
RL   J. Mol. Biol. 332:369-383(2003).
CC   -!- FUNCTION: This protein is essential for replication of the
CC       chromosome. It is also involved in DNA recombination and repair
CC       (By similarity).
CC   -!- SIMILARITY: Contains 1 SSB domain.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AY305378; AAP86084.1; -.
DR   PROSITE; PS50935; SSB; 1.
KW   DNA-binding; DNA repair; DNA replication; Plasmid.
FT   DOMAIN        4    109       SSB.
SQ   SEQUENCE   188 AA;  20451 MW;  B43832FBCC232CF4 CRC64;

  Query Match             12.9%;  Score 78.5;  DB 1;  Length 188;
  Best Local Similarity   33.8%;  Pred. No. 0.71;
  Matches   26;  Conservative    8;  Mismatches   30;  Indels   13;  Gaps    5;

Qy          32 GTGGAATTMGNSCICRDDSGTDDSVDTQQQQAENSAVPTADTRSQP--RDPVRPPRRGRG 89
               | |||:   |:|     |||||  |    |   :  :||   |  |  | | :||  | |
Db         110 GRGGASD--GDS-----DSGTDRSASQQSPASAQRSAPTGQ-RQPPARRQPAQPPSNGFG 161

Qy          90 PHE---PRRKKQNVDGL 103
                  |   :  :||:
Db         162 DFNEDIPFARPAALDGI 178


RESULT 3
BA1B_HUMAN
ID   BA1B_HUMAN     STANDARD;      PRT;  1483 AA.
AC   Q9UIG0; O95039; O95247; O95277;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Bromodomain adjacent to zinc finger domain protein 1B (Williams-Beuren
DE   syndrome chromosome region 9 protein) (WBRS9) (Williams syndrome
DE   transcription factor) (hWALP2).
GN   BAZ1B OR WBSCR9 OR WBSC10 OR WSTF.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RX   MEDLINE=99077764; PubMed=9858827;
RA   Peoples R.J., Cisco M.J., Kaplan P., Francke U.;
RT   "Identification of the WBSCR9 gene, encoding a novel transcriptional
RT   regulator, in the Williams-Beuren syndrome deletion at 7q11.23.";
RL   Cytogenet. Cell Genet. 82:238-246(1998).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RX   MEDLINE=99047530; PubMed=9828126;
RA   Lu X., Meng X., Morris C.A., Keating M.T.;
RT   "A novel human gene, WSTF, is deleted in Williams Syndrome.";
RL   Genomics 54:241-249(1998).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC   TISSUE=Testis;
RX   MEDLINE=20130112; PubMed=10662543;
RA   Jones M.H., Hamana N., Nezu J., Shimane M.;
RT   "A novel family of bromodomain genes.";
RL   Genomics 63:40-45(2000).
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Minx P., Graves T., Duckels G., Harrison M., Waterston R.;
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   FUNCTION.
RX   MEDLINE=21977304; PubMed=11980720;
RA   Bozhenok L., Wade P.A., Varga-Weisz P.;
RT   "WSTF-ISWI chromatin remodeling complex targets heterochromatic
RT   replication foci.";
RL   EMBO J. 21:2231-2241(2002).
CC   -!- FUNCTION: Forms a chromatin remodeling complex that mobilizes
CC       nucleosomes and reconfigures irregular chromatin to a regular
CC       nucleosomal array structure.
CC   -!- SUBUNIT: Interacts with ISWI (imitation SWI protein) to form the
CC       WSTF-ISWI chromatin remodeling complex (WICH).
CC   -!- SUBCELLULAR LOCATION: Nuclear (Potential). Accumulates in
CC       pericentromeric heterochromatin during replication.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1;
CC         IsoId=Q9UIG0-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=Q9UIG0-2; Sequence=VSP_000552;
CC   -!- TISSUE SPECIFICITY: Ubiquitously expressed with high levels of
CC       expression in heart, brain, placenta, skeletal muscle and ovary.
CC   -!- DEVELOPMENTAL STAGE: Expressed at equal levels in 19-23 weeks old
CC       fetal tissues.
CC   -!- DISEASE: Haploinsufficiency of BAZ1B may be the cause of certain
CC       cardiovascular and musculo-skeletal abnormalities observed in
CC       Williams-Beuren syndrome (WBS), a rare developmental disorder. It
CC       is a contiguous gene deletion syndrome involving genes from
CC       chromosome band 7q11.23.
CC   -!- SIMILARITY: Belongs to the WAL family.
CC   -!- SIMILARITY: Contains 1 bromodomain.
CC   -!- SIMILARITY: Contains 1 DDT domain.
CC   -!- SIMILARITY: Contains 1 PHD-type zinc finger.
CC   -!- SIMILARITY: Contains 1 WAC domain.
CC   -!- CAUTION: Ref.2 sequence differs from that shown due to frameshifts
CC       in positions 1031, 1042 and 1422.
CC   -!- CAUTION: Ref.3 sequence differs from that shown due to a
CC       frameshift in position 1478.
CC   -!- CAUTION: Ref.4 sequence differs from that shown due to erroneous
CC       gene model prediction.
CC   ---------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; AF084479; AAD08675.1; -.
DR   EMBL; AF072810; AAC97879.1; ALT_FRAME.
DR   EMBL; AB032253; BAA89210.1; ALT_FRAME.
DR   EMBL; AC005074; AAD04720.1; ALT_SEQ.
DR   EMBL; AC005089; -; NOT_ANNOTATED_CDS.
DR   HSSP; Q92831; 1B91.
DR   TRANSFAC; T04145; -.
DR   Genew; HGNC:961; BAZ1B.
DR   MIM; 605681; -.
DR   GO; GO:0005634; C:nucleus; NAS.
DR   GO; GO:0003700; F:transcription factor activity; NAS.
DR   GO; GO:0008270; F:zinc ion binding; NAS.
DR   GO; GO:0006350; P:transcription; NAS.
DR   InterPro; IPR001487; Bromodomain.
DR   InterPro; IPR004022; DDT_dom.
DR   InterPro; IPR001965; Znf_PHD.
DR   Pfam; PF00439; bromodomain; 1.
DR   Pfam; PF00628; PHD; 1.
DR   PRINTS; PR00503; BROMODOMAIN.
DR   SMART; SM00297; BROMO; 1.
DR   SMART; SM00571; DDT; 1.
DR   SMART; SM00249; PHD; 1.
DR   PROSITE; PS00633; BROMODOMAIN_1; FALSE_NEG.
DR   PROSITE; PS50014; BROMODOMAIN_2; 1.
DR   PROSITE; PS50827; DDT; 1.
DR   PROSITE; PS01359; ZF_PHD_1; 1.
DR   PROSITE; PS50016; ZF_PHD_2; 1.
KW   Transcription regulation; Bromodomain; Zinc-finger; Coiled coil;
KW   Nuclear protein; Alternative splicing; Williams-Beuren syndrome.
FT   DOMAIN       20    126       WAC.
FT   DOMAIN      604    668       DDT.
FT   ZN_FING    1184   1234       PHD-TYPE.
FT   DOMAIN     1356   1426       BROMODOMAIN.
FT   DOMAIN      306    578       LYS-RICH.
FT   DOMAIN      533    586       COILED COIL (POTENTIAL).
FT   DOMAIN      768    814       COILED COIL (POTENTIAL).
FT   DOMAIN      850    893       COILED COIL (POTENTIAL).
FT   DOMAIN     1245   1283       COILED COIL (POTENTIAL).
FT   DOMAIN     1261   1273       POLY-GLU.
FT   VARSPLIC    660    663       Missing (in isoform 2).
FT                                /FTId=VSP_000552.
FT   CONFLICT     14     14       K -> N (IN REF. 3).
FT   CONFLICT     22     22       L -> F (IN REF. 3).
FT   CONFLICT    136    136       K -> E (IN REF. 1).
FT   CONFLICT    191    191       N -> D (IN REF. 4).
FT   CONFLICT    298    298       Y -> V (IN REF. 4).
FT   CONFLICT    823    823       E -> R (IN REF. 3).
FT   CONFLICT   1191   1191       R -> P (IN REF. 3).
FT   CONFLICT   1354   1354       K -> M (IN REF. 2).
FT   CONFLICT   1438   1438       A -> V (IN REF. 3).
SQ   SEQUENCE   1483 AA;  170902 MW;  0CC146FEBB954261 CRC64;

  Query Match             12.8%;  Score 78;  DB 1;  Length 1483;
  Best Local Similarity   27.5%;  Pred. No. 8;
  Matches   22;  Conservative   12;  Mismatches   26;  Indels   20;  Gaps    3;

Qy         48 DDSGTDDSVDTQQQQAENSAVPTADTRSQPRDPVR------PP------RRGRGPHEPRR 95
              :|  :|:  : ::::: |       |  | :||  :|      ||      | |: ||  ||
Db       1255 EDDESDEEEEEEEEEEEEEDYEVAGLRLRPRKTIRGKHSVIPPAARSGRRPGKKPHSTRR 1314

Qy         96 KK--------QNVDGLVLDT 107
                :          || |||  |
Db       1315 SQPKAPPVDDAEVDELVLQT 1334

RESULT 4
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MSA2_PLAF1
ID   MSA2_PLAF1     STANDARD;      PRT;   286 AA.
AC   P50496;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
DE   Merozoite surface antigen 2 precursor (MSA-2).
GN   MSA2.
OS   Plasmodium falciparum (isolate 311).
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=57265;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92178286; PubMed=1542312;
RA   Marshall V.M., Coppel R.L., Anders R.F., Kemp D.J.;
RT   "Two novel alleles within subfamilies of the merozoite surface
RT   antigen 2 (MSA-2) of Plasmodium falciparum.";
RL   Mol. Biochem. Parasitol. 50:181-184(1992).
CC   -!- FUNCTION: May play a role in the merozoite attachment to the
CC       erythrocyte.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC       (Potential).
CC   -!- DEVELOPMENTAL STAGE: During the trophozoite and schizont stages.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; M73809; AAA29697.1; -.
DR   InterPro; IPR001136; MSA_2.
DR   Pfam; PF00985; MSA_2; 1.
KW   Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;
KW   GPI-anchor; Merozoite.
FT   SIGNAL       1     20       POTENTIAL.
FT   CHAIN       21    262       MEROZOITE SURFACE ANTIGEN 2.
FT   PROPEP     263    286       HYDROPHOBIC, REMOVED DURING MATURATION
FT                               (BY SIMILARITY).
FT   DOMAIN      44    212       POLYMORPHIC REGION.
FT   DOMAIN     115    122       POLY-THR.
FT   CARBOHYD    22     22       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    36     36       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   163    163       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   235    235       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   259    259       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   260    260       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   286 AA;  28844 MW;  D1F4947CE68D5805 CRC64;

  Query Match             12.3%;  Score 75;  DB 1;  Length 286;
  Best Local Similarity   34.6%;  Pred. No. 2.5;
  Matches   27;  Conservative    6;  Mismatches   25;  Indels   20;  Gaps    5;

Qy         32 GTGGA-------ATTMGNSCICRDDSGTDDSV------DT-----QQQQAENSAVPTADT 73
              | ||          |  || : : || |  :|      ||     | :|||||| |||:
Db        147 GNGGVQKPNQANKETQNNSNV-QQDSQTKSNVPPTQDADTKSPTAQPEQAENSA-PTAEQ 204

Qy         74 RSQPRDPVRPPRRGRGPH 91
                 |     |  :| | |
Db        205 TESPELQSAPENKGTGQH 222


RESULT 5
CCAA_HUMAN
ID   CCAA_HUMAN     STANDARD;      PRT;  2505 AA.
AC   O00555; P78510; P78511; Q16290; Q92690; Q99790; Q99791; Q99792;
AC   Q99793;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Voltage-dependent P/Q-type calcium channel alpha-1A subunit (Calcium
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DE   channel, L type, alpha-1 polypeptide isoform 4) (Brain calcium channel
DE   I) (BI).
GN   CACNA1A OR CACNL1A4 OR CACH4 OR CACN3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS BI-1-GGCAG/1A-1 AND BI-1/1A-2).
RC   TISSUE=Neuron;
RX   MEDLINE=99158614; PubMed=10049321;
RA   Hans M., Urrutia A., Deal C., Brust P.F., Stauderman K., Ellis S.B.,
RA   Harpold M.M., Johnson E.C., Williams M.E.;
RT   "Structural elements in domain IV that influence biophysical and
RT   pharmacological properties of human alpha1A-containing high-voltage-
RT   activated calcium channels.";
RL   Biophys. J. 76:1384-1400(1999).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM BI-1(V1)), AND VARIANTS FHM.
RC   TISSUE=Cerebellum;
RX   MEDLINE=97053792; PubMed=8898206;
RA   Ophoff R.A., Terwindt G.M., Vergouwe M.N., van Eijk R., Oefner P.J.,
RA   Hoffman S.M.G., Lamerdin J.E., Mohrenweiser H.W., Bulman D.E.,
RA   Ferrari M., Haan J., Lindhout D., van Ommen G.-J.B., Hofker M.H.,
RA   Ferrari M.D., Frants R.R.;
RT   "Familial hemiplegic migraine and episodic ataxia type-2 are caused by
RT   mutations in the Ca2+ channel gene CACNL1A4.";
RL   Cell 87:543-552(1996).
RN   [3]
RP   SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC   TISSUE=Brain;
RX   MEDLINE=97141920; PubMed=8988170;
RA   Zhuchenko O., Bailey J., Bonnen P.E., Ashizawa T., Stockton D.W.,
RA   Amos C., Dobyns W.B., Subramony S.H., Zoghbi H.Y., Lee C.C.;
RT   "Autosomal dominant cerebellar ataxia (SCA6) associated with small
RT   polyglutamine expansions in the alpha 1A-voltage-dependent calcium
RT   channel.";
RL   Nat. Genet. 15:62-69(1997).
RN   [4]
RP   SEQUENCE OF 1233-1651 FROM N.A.
RA   Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,
RA   Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S.,
RA   Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,
RA   Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
RA   Liu S., Attix C., Andreise T., Trankheim M., Amico-Keller G.,
RA   Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
RA   Kronmiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,
RA   Kobayashi A., Olsen A.S., Carrano A.V.;
RL   Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE OF 1693-1807 FROM N.A.
RC   TISSUE=Lung carcinoma;
RX   MEDLINE=95123449; PubMed=7823133;
RA   Barry E.L.R., Viglione M.P., Kim Y.I., Froehner S.C.;
RT   "Expression and antibody inhibition of P-type calcium channels in
RT   human small-cell lung carcinoma cells.";
RL   J. Neurosci. 15:274-283(1995).
RN   [6]
RP   SEQUENCE OF 2038-2258 FROM N.A.
RC   TISSUE=Frontal cortex;
RX   MEDLINE=96102310; PubMed=8525433;
RA   Margolis R.L., Breschel T.S., Li S.H., Kidwai A.S., Antonarakis S.E.,
RA   McInnis M.G., Ross C.A.;
RT   "Characterization of cDNA clones containing CCA trinucleotide repeats
RT   derived from human brain.";
RL   Somat. Cell Mol. Genet. 21:279-284(1995).
CC   -!- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the
CC       entry of calcium ions into excitable cells and are also involved
CC       in a variety of calcium-dependent processes, including muscle
CC       contraction, hormone or neurotransmitter release, gene expression,
CC       cell motility, cell division and cell death. The isoform alpha-1A
CC       gives rise to P and/or Q-type calcium currents. P/Q-type calcium
CC       channels belong to the "high-voltage activated" (HVA) group and
CC       are blocked by the funnel toxin (Ftx) and by the omega-agatoxin-
CC       IVA (omega-Aga-IVA). They are however insensitive to
CC       dihydropyridines (DHP), and omega-conotoxin-GVIA (omega-CTx-GVIA).
CC   -!- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT
CC       COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS
CC       IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-
CC       FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS
CC       SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM
CC       CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA
CC       LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=7;
CC         Comment=Additional isoforms seem to exist;
CC       Name=BI-1-GGCAG; Synonyms=1A-1;
CC         IsoId=O00555-1; Sequence=Displayed;
CC       Name=BI-1; Synonyms=1A-2;
CC         IsoId=O00555-2; Sequence=VSP_000875;
CC       Name=BI-1(V1);
CC         IsoId=O00555-3; Sequence=VSP_000871, VSP_000875;
CC       Name=BI-1(V1)-GGCAG;
CC         IsoId=O00555-4; Sequence=VSP_000871;
CC       Name=BI-1(V2);
CC         IsoId=O00555-5; Sequence=VSP_000872;
CC       Name=BI-1(V2)-GGCAG;
CC         IsoId=O00555-6; Sequence=VSP_000872;
CC       Name=BI-1(V2,V3);
CC         IsoId=O00555-7; Sequence=VSP_000873, VSP_000874;
CC   -!- TISSUE SPECIFICITY: Brain specific; mainly found in cerebellum,
CC       cerebral cortex, thalamus and hypothalamus. No expression in
CC       heart, kidney, liver or muscle. Purkinje cells contain
CC       predominantly P-type VSCC, the Q-type being a prominent calcium
CC       current in cerebellar granule cells.
CC   -!- DOMAIN: Each of the four internal repeats contains five
CC       hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one
CC       positively charged transmembrane segment (S4). S4 segments
CC       probably represent the voltage-sensor and are characterized by a
CC       series of positively charged amino acids at every third position.
CC   -!- POLYMORPHISM: The poly-Gln region of CACNA1A is polymorphic: 6 to
CC       17 repeats in the normal population, expanded to about 21 to 30
CC       repeats in spinocerebellar ataxia 6 (SCA6) patients. There seems
CC       to be a correlation between the repeat number and earlier onset of
CC       the disorder.
CC   -!- DISEASE: Defects in CACNA1A are the cause of spinocerebellar
CC       ataxia type 6 (SCA6) [MIM:183086]. SCA6 is an autosomal dominant
CC       disorder characterized by slowly progressive cerebellar ataxia of
CC       the limbs and gait, dysarthria, nystagmus, and mild vibratory and
CC       proprioceptive sensory loss. These symptoms are probably explained
CC       by severe loss of cerebellar Purkinje cells. SCA6 is cause by
CC       expansion of a CAG repeat in the coding region of CACNA1A.
CC   -!- DISEASE: Defects in CACNA1A are the cause of familial hemiplegic
CC       migraine (FHM) [MIM:141500]; also known as migraine familial
CC       hemiplegic 1 (MHP1). FHM, a rare autosomal dominant subtype of
CC       migraine with aura, is associated with ictal hemiparesis and, in
CC       some families, progressive cerebellar atrophy.
CC   -!- DISEASE: Defects in CACNA1A are the cause of episodic ataxia type
CC       2 (EA-2) [MIM:108500]; also known as acetazolamide-responsive
CC       hereditary paroxysmal cerebellar ataxia (APCA). This autosomal
CC       dominant disorder is characterized by acetozolamide-responsive
CC       attacks of cerebellar ataxia and migraine-like symptoms,
CC       interictal nystagmus, and cerebellar atrophy.
CC   -!- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
CC       family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF004884; AAB61613.1; -.
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DR   EMBL; AF004883; AAB61612.1; -.
DR   EMBL; X99897; CAA68172.1; -.
DR   EMBL; Z80114; -; NOT_ANNOTATED_CDS.
DR   EMBL; Z80115; -; NOT_ANNOTATED_CDS.
DR   EMBL; U79666; AAB64179.1; -.
DR   EMBL; U79663; AAB49674.1; ALT_INIT.
DR   EMBL; U79664; AAB49675.1; ALT_INIT.
DR   EMBL; U79665; AAB49676.1; ALT_INIT.
DR   EMBL; U79667; AAB49677.1; ALT_INIT.
DR   EMBL; U79668; AAB49678.1; ALT_INIT.
DR   EMBL; AC005305; AAC26839.1; -.
DR   EMBL; S76537; AAB33068.1; -.
DR   EMBL; U06702; -; NOT_ANNOTATED_CDS.
DR   Genew; HGNC:1388; CACNA1A.
DR   MIM; 601011; -.
DR   MIM; 183086; -.
DR   MIM; 141500; -.
DR   MIM; 108500; -.
DR   GO; GO:0007399; P:neurogenesis; TAS.
DR   GO; GO:0007268; P:synaptic transmission; TAS.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002077; Ca_channel_alpha.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR005448; PQVDCCAlpha1.
DR   Pfam; PF00520; ion_trans; 4.
DR   PRINTS; PR00167; CACHANNEL.
DR   PRINTS; PR01632; PQVDCCALPHA1.
KW   Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW   Calcium channel; Glycoprotein; Repeat; Multigene family;
KW   Calcium-binding; Phosphorylation; Alternative splicing; Polymorphism;
KW   Disease mutation; Triplet repeat expansion.
FT   REPEAT       85    363       I.
FT   REPEAT      473    717       II.
FT   REPEAT     1231   1514       III.
FT   REPEAT     1551   1814       IV.
FT   DOMAIN        1     98       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     99    117       S1 OF REPEAT I (POTENTIAL).
FT   DOMAIN      118    135       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    136    155       S2 OF REPEAT I (POTENTIAL).
FT   DOMAIN      156    167       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    168    185       S3 OF REPEAT I (POTENTIAL).
FT   DOMAIN      186    190       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    191    209       S4 OF REPEAT I (POTENTIAL).
FT   DOMAIN      210    228       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    229    248       S5 OF REPEAT I (POTENTIAL).

  Query Match             12.1%;  Score 73.5;  DB 1;  Length 2505;
  Best Local Similarity   24.2%;  Pred. No. 41;
  Matches   31;  Conservative    9;  Mismatches   39;  Indels   49;  Gaps    4;

Qy          12 SRSLGQGLLLTLEEHIAHFLGTGG-----AATTMGNSC---------------------- 44
               |||  :|      ||:||  |:       | :| | |
Db        2247 SRSPSEG-----REHMAHRQGSSSVSGSPAPSTSGTSTPRRGRRQLPQTPSTPRPHVSYS 2301

Qy          45 -ICRDDSGTDDSVDTQQQQAENSAV----------------PTADTRSQPRDPVRPPRRG 87
                : |   |:       |||| :  ||                |||:  :  | |      |
Db        2302 PVIRKAGGSGPPQQQQQQQQQQQAVARPGRAATSGPRRYPGPTAEPLAGDRPPTGGHSSG 2361

Qy          88 RGPHEPRR 95
               | |   ||
Db        2362 RSPRMERR 2369


RESULT 6
MSA2_PLAFH
ID   MSA2_PLAFH     STANDARD;      PRT;   281 AA.
AC   Q99319;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
DE   Merozoite surface antigen 2 precursor (MSA-2) (Allelic form 3).
GN   MSA2.
OS   Plasmodium falciparum (isolate thtn / Thailand).
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=70151;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91218803; PubMed=2090943;
RA   Thomas A.W., Carr D.A., Carter J.M., Lyon J.A.;
RT   "Sequence comparison of allelic forms of the Plasmodium falciparum
RT   merozoite surface antigen MSA2.";
RL   Mol. Biochem. Parasitol. 43:211-220(1990).
CC   -!- FUNCTION: May play a role in the merozoite attachment to the
CC       erythrocyte.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC       (Potential).
CC   -!- DEVELOPMENTAL STAGE: During the trophozoite and schizont stages.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M60189; AAA29689.1; -.
DR   InterPro; IPR001136; MSA_2.
DR   Pfam; PF00985; MSA_2; 1.
KW   Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;
KW   GPI-anchor; Merozoite.
FT   SIGNAL        1     20       POTENTIAL.
FT   CHAIN        21    257       MEROZOITE SURFACE ANTIGEN 2.
FT   PROPEP      258    281       HYDROPHOBIC, REMOVED DURING MATURATION
FT                                (BY SIMILARITY).
FT   DOMAIN       44    207       POLYMORPHIC REGION.
FT   DOMAIN      111    118       POLY-THR.
FT   CARBOHYD     22     22       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     36     36       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    158    158       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    230    230       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    254    254       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    255    255       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   281 AA;  28892 MW;  50598AA42D64CCBC CRC64;

  Query Match             12.0%;  Score 73;  DB 1;  Length 281;
  Best Local Similarity   35.8%;  Pred. No. 4;
  Matches   24;  Conservative    6;  Mismatches   25;  Indels   12;  Gaps    3;

Qy          36 AATTMGNSCICRDDSGTDDSV------DT-----QQQQAENSAVPTADTRSQPRDPVRPP 84
               | |   |:   : || |  :|       ||     | :|||||| |||:    |      |
Db         152 ANTETQNNSNVQQDSQTKSNVPPTQDADTKSPTAQPEQAENSA-PTAEQTESPELQSAPE 210

Qy          85 RRGRGPH 91
               :| | |
Db         211 NKGTGQH 217


RESULT 7
TGN1_MOUSE
ID   TGN1_MOUSE     STANDARD;      PRT;   353 AA.
AC   Q62313;
DT   15-MAR-2004 (Rel. 43, Created)
DT   15-MAR-2004 (Rel. 43, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Trans-golgi network integral membrane protein 1 precursor (TGN38A).
GN   TGOLN1 OR TTGN1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ICR; TISSUE=Brain;
```

```
RX   MEDLINE=95301533; PubMed=7540170;
RA   Kasai K., Takahashi S., Murakami K., Nakayama K.;
RT   "Strain-specific presence of two TGN38 isoforms and absence of TGN41
RT   in mouse.";
RL   J. Biol. Chem. 270:14471-14476(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Aorta, and Testis;
RX   MEDLINE=22354683; PubMed=12466851;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: May be involved in regulating membrane traffic to and
CC       from trans-Golgi network.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Primarily in trans-
CC       Golgi network. Cycles between the trans-Golgi network and the cell
CC       surface returning via endosomes (By similarity).
CC   -!- TISSUE SPECIFICITY: Widely expressed.
CC   -!- MISCELLANEOUS: Also found in strains BALB/c, C57BL/6 and DBA/2.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; D50031; BAA08757.1; -.
DR   EMBL; AK041302; BAC30896.1; -.
DR   EMBL; AK076586; BAC36404.1; -.
DR   EMBL; BC009143; AAH09143.1; -.
DR   PIR; B56940; B56940.
DR   MGD; MGI:105080; Tgoln1.
KW   Signal; Transmembrane; Glycoprotein; Repeat; Golgi stack.
FT   SIGNAL       1     17       POTENTIAL.
FT   CHAIN       18    353       TRANS-GOLGI NETWORK INTEGRAL MEMBRANE
FT                               PROTEIN 1.
FT   DOMAIN      18    298       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   299    319       POTENTIAL.
FT   DOMAIN     320    353       CYTOPLASMIC (POTENTIAL).
FT   SITE       346    349       ENDOCYTOSIS SIGNAL (BY SIMILARITY).
FT   DOMAIN     131    178       6 X 8 AA TANDEM REPEATS.
FT   REPEAT     131    138       1.
FT   REPEAT     139    146       2.
FT   REPEAT     147    154       3.
FT   REPEAT     155    162       4.
FT   REPEAT     163    170       5.
FT   REPEAT     171    178       6.
FT   CARBOHYD   110    110       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   293    293       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   353 AA;  37848 MW;  95C340C2F4A21EB3 CRC64;

  Query Match             12.0%;  Score 73;  DB 1;  Length 353;
  Best Local Similarity   30.5%;  Pred. No. 5.1;
  Matches   18;  Conservative    9;  Mismatches   28;  Indels    4;  Gaps    1;

Qy         32 GTGGAATTMGNSCICRDDSGTDDSVDTQQQQAENSAVPTADTRSQPRDPVRPPRRGRGP 90
              |  |  |  |::    ||||     ||  :  :: |     || :   | |:|  :|: |
Db        148 GDSGKPTEAGSNKATEDDSGKSTKVDLDKPTSKIS----PDTETSKTDKVQPTEKGQKP 202


RESULT 8
CA13_HUMAN
ID   CA13_HUMAN     STANDARD;      PRT;  1466 AA.
AC   P02461; Q15112;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Collagen alpha 1(III) chain precursor.
GN   COL3A1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skin fibroblast;
RX   MEDLINE=89350838; PubMed=2764886;
RA   Ala-Kokko L., Kontusaari S., Baldwin C.T., Kuivaniemi H.,
RA   Prockop D.J.;
RT   "Structure of cDNA clones coding for the entire prepro alpha 1 (III)
RT   chain of human type III procollagen. Differences in protein structure
RT   from type I procollagen and conservation of codon preferences.";
RL   Biochem. J. 260:509-516(1989).
RN   [2]
RP   SEQUENCE OF 149-1225 FROM N.A.
RX   MEDLINE=89386015; PubMed=2780304;
RA   Janeczko R.A., Ramirez F.;
RT   "Nucleotide and amino acid sequences of the entire human alpha 1
RT   (III) collagen.";
RL   Nucleic Acids Res. 17:6742-6742(1989).
RN   [3]
RP   SEQUENCE OF 168-398.
RX   MEDLINE=77134724; PubMed=557335;
RA   Seyer J.M., Kang A.H.;
RT   "Covalent structure of collagen: amino acid sequence of cyanogen
```

RT bromide peptides from the amino-terminal segment of type III collagen
RT of human liver.";
RL Biochemistry 16:1158-1164(1977).
RN [4]
RP REVISIONS.
RA Seyer J.M.;
RL Submitted (DEC-1977) to the PIR data bank.
RN [5]
RP SEQUENCE OF 399-727.
RX MEDLINE=79000343; PubMed=687591;
RA Seyer J.M., Kang A.H.;
RT "Covalent structure of collagen: amino acid sequence of five
RT consecutive CNBr peptides from type III collagen of human liver.";
RL Biochemistry 17:3404-3411(1978).
RN [6]
RP SEQUENCE OF 728-964.
RX MEDLINE=80198282; PubMed=6246925;
RA Seyer J.M., Mainardi C., Kang A.H.;
RT "Covalent structure of collagen: amino acid sequence of alpha 1
RT (III)-CB5 from type III collagen of human liver.";
RL Biochemistry 19:1583-1589(1980).
RN [7]
RP SEQUENCE OF 950-1466 FROM N.A.
RX MEDLINE=88189827; PubMed=3357782;
RA Mankoo B.S., Dalgleish R.;
RT "Human pro alpha 1(III) collagen: cDNA sequence for the 3' end.";
RL Nucleic Acids Res. 16:2337-2337(1988).
RN [8]
RP REVISION TO 1184.
RX MEDLINE=89098346; PubMed=3211760;
RA Molyneux K., Dalgleish R.;
RT "Human type III collagen 'variant' is a cDNA cloning artefact.";
RL Nucleic Acids Res. 16:11833-11833(1988).
RN [9]
RP SEQUENCE OF 1065-1466 FROM N.A.
RX MEDLINE=85087944; PubMed=6096827;
RA Loidl H.R., Brinker J.M., May M., Pihlajaniemi T., Morrow S.,
RA Rosenbloom J., Myers J.C.;
RT "Molecular cloning and carboxyl-propeptide analysis of human type III
RT procollagen.";
RL Nucleic Acids Res. 12:9383-9394(1984).
RN [10]
RP SEQUENCE OF 965-1200.
RX MEDLINE=81208139; PubMed=7016180;
RA Seyer J.M., Kang A.H.;
RT "Covalent structure of collagen: amino acid sequence of alpha
RT 1(III)-CB9 from type III collagen of human liver.";
RL Biochemistry 20:2621-2627(1981).
RN [11]
RP SEQUENCE OF 1176-1466 FROM N.A.
RX MEDLINE=85157600; PubMed=2579949;
RA Chu M.-L., Weil D., de Wet W.J., Bernard M.P., Sippola M., Ramirez F.;
RT "Isolation of cDNA and genomic clones encoding human pro-alpha 1
RT (III) collagen. Partial characterization of the 3' end region of the
RT gene.";
RL J. Biol. Chem. 260:4357-4363(1985).
RN [12]
RP SEQUENCE OF 1161-1200 FROM N.A.
RX MEDLINE=86187804; PubMed=3754462;
RA Miskulin M., Dalgleish R., Kluve-Beckerman B., Rennard S.I.,
RA Tolstoshev P., Brantly M., Crystal R.G.;
RT "Human type III collagen gene expression is coordinately modulated
RT with the type I collagen genes during fibroblast growth.";
RL Biochemistry 25:1408-1413(1986).
RN [13]
RP SEQUENCE OF 1-170 FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=88303360; PubMed=3405773;
RA Toman D., Ricca G., de Crombrugghe B.;
RT "Nucleotide sequence of a cDNA coding for the amino-terminal region
RT of human prepro alpha 1(III) collagen.";
RL Nucleic Acids Res. 16:7201-7201(1988).
RN [14]
RP SEQUENCE OF 1-176 FROM N.A.
RX MEDLINE=89378752; PubMed=2777083;
RA Benson-Chanda V., Su M.W., Weil D., Chu M.-L., Ramirez F.;
RT "Cloning and analysis of the 5' portion of the human type-III
RT procollagen gene (COL3A1).";
RL Gene 78:255-265(1989).
RN [15]
RP REVIEW ON VARIANTS.
RX MEDLINE=97255959; PubMed=9101290;
RA Kuivaniemi H., Tromp G., Prockop D.J.;
RT "Mutations in fibrillar collagens (types I, II, III, and XI), fibril-
RT associated collagen (type IX), and network-forming collagen (type X)
RT cause a spectrum of diseases of bone, cartilage, and blood vessels.";
RL Hum. Mutat. 9:300-315(1997).
RN [16]
RP VARIANT AORTIC ANEURYSM ARG-303, AND VARIANT THR-668.
RX MEDLINE=93293988; PubMed=8514866;
RA Tromp G., Wu Y., Prockop D.J., Madhatheri S.L., Kleinert C.,
RA Earley J.J., Zhuang J., Noerrgaard O., Darling R.C., Abbott W.M.,
RA Cole C.W., Jaakkola P., Ryynaenen M., Pearce W.H., Yao J.S.T.,
RA Majamaa K., Smullens S.N., Gatalica Z., Ferrell R.E., Jimenez S.A.,
RA Jackson C.E., Michels V.V., Kaye M., Kuivaniemi H.;
RT "Sequencing of cDNA from 50 unrelated patients reveals that mutations
RT in the triple-helical domain of type III procollagen are an
RT infrequent cause of aortic aneurysms.";
RL J. Clin. Invest. 91:2539-2545(1993).
RN [17]
RP VARIANT THR-698.
RX MEDLINE=91045136; PubMed=2235526;
RA Zafarullah K., Kleinert C., Tromp G., Kuivaniemi H., Kontusaari S.,
RA Wu Y., Ganguly A., Prockop D.J.;
RT "G to A polymorphism in exon 31 of the COL3A1 gene.";
RL Nucleic Acids Res. 18:6180-6180(1990).
RN [18]
RP VARIANT AORTIC ANEURYSM ARG-786.
RX MEDLINE=91056145; PubMed=2243125;
RA Kontusaari S., Tromp G., Kuivaniemi H., Romanic A.M., Prockop D.J.;
RT "A mutation in the gene for type III procollagen (COL3A1) in a family
RT with aortic aneurysms.";
RL J. Clin. Invest. 86:1465-1473(1990).
RN [19]
RP VARIANT EDS-IV ARG-828.
RX MEDLINE=94016385; PubMed=8411057;
RA Richards A.J., Narcisi P., Lloyd J.C., Ferguson C., Pope F.M.;
RT "The substitution of glycine 661 by arginine in type III collagen
RT produces mutant molecules with different thermal stabilities and
RT causes Ehlers-Danlos syndrome type IV.";
RL J. Med. Genet. 30:690-693(1993).
RN [20]
RP VARIANT EDS-IV SER-957.
RX MEDLINE=89109135; PubMed=2492273;
RA Tromp G., Kuivaniemi H., Shikata H., Prockop D.J.;
RT "A single base mutation that substitutes serine for glycine 790 of
RT the alpha 1 (III) chain of type III procollagen exposes an arginine
RT and causes Ehlers-Danlos syndrome IV.";
RL J. Biol. Chem. 264:1349-1352(1989).
RN [21]
RP VARIANT EDS-IV VAL-960.
RX MEDLINE=95268429; PubMed=7749417;
RA Tromp G., de Paepe A., Nuytinck L., Madhatheri S.L., Kuivaniemi H.;
RT "Substitution of valine for glycine 793 in type III procollagen in
RT Ehlers-Danlos syndrome type IV.";
RL Hum. Mutat. 5:179-181(1995).
RN [22]
RP VARIANT EDS-IV GLU-1014.
RX MEDLINE=92316511; PubMed=1352273;
RA Richards A.J., Ward P.N., Narcisi P., Nicholls A.C., Lloyd J.C.,
RA Pope F.M.;
RT "A single base mutation in the gene for type III collagen (COL3A1)
RT converts glycine 847 to glutamic acid in a family with Ehlers-Danlos
RT syndrome type IV. An unaffected family member is mosaic for the
RT mutation.";
RL Hum. Genet. 89:414-418(1992).

```
RN   [23]
RP   VARIANT EDS-IV ASP-1050.
RX   MEDLINE=90037070; PubMed=2808425;
RA   Tromp G., Kuivaniemi H., Stolle C.A., Pope F.M., Prockop D.J.;
RT   "Single base mutation in the type III procollagen gene that converts
RT   the codon for glycine 883 to aspartate in a mild variant of
RT   Ehlers-Danlos syndrome IV.";
RL   J. Biol. Chem. 264:19313-19317(1989).
RN   [24]
RP   VARIANT EDS-IV VAL-1077.
RX   MEDLINE=91374480; PubMed=1895316;
RA   Richards A.J., Lloyd J.C., Ward P.N., de Paepe A., Narcisi P.,
RA   Pope F.M.;
RT   "Characterisation of a glycine to valine substitution at amino acid
RT   position 910 of the triple helical region of type III collagen in a
RT   patient with Ehlers-Danlos syndrome type IV.";
RL   J. Med. Genet. 28:458-463(1991).
RN   [25]
RP   VARIANT EDS-IV GLU-1173.
RX   MEDLINE=93022543; PubMed=1357232;
RA   Johnson P.H., Richards A.J., Pope F.M., Hopkinson D.A.;

  Query Match             12.0%;  Score 73;  DB 1;  Length 1466;
  Best Local Similarity   28.8%;  Pred. No. 25;
  Matches   30;  Conservative   10;  Mismatches   36;  Indels   28;  Gaps    7;

Qy          16 GQGLLLTLEEH---IAHFLGTGGAATTMGNS--------------CICRDDSGT---DDS 55
               |  ||| |       :|     |   : :| |              |:|  |||:   ||
Db           8 GSWLLLALLHPTIILAQQEAVEGGCSHLGQSYADRDVWKPEPCQICVC--DSGSVLCDDI 65

Qy          56 V-DTQQQQAENSAVP----TADTRSQPRDPVRPPRRGRGPHEPR 94
               : | |:    |  :|    |     |  | |||  |:||  |:
Db          66 ICDDQELDCPNPEIPFGECCAVCPQPPTAPTRPP-NGQGPQGPK 108


RESULT 9
MSA2_PLAFC
ID   MSA2_PLAFC     STANDARD;      PRT;   262 AA.
AC   Q99317;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
DE   Merozoite surface antigen 2 precursor (MSA-2) (Allelic form 1).
GN   MSA2.
OS   Plasmodium falciparum (isolate Camp / Malaysia).
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5835;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91218803; PubMed=2090943;
RA   Thomas A.W., Carr D.A., Carter J.M., Lyon J.A.;
RT   "Sequence comparison of allelic forms of the Plasmodium falciparum
RT   merozoite surface antigen MSA2.";
RL   Mol. Biochem. Parasitol. 43:211-220(1990).
CC   -!- FUNCTION: May play a role in the merozoite attachment to the
CC       erythrocyte.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC       (Potential).
CC   -!- DEVELOPMENTAL STAGE: During the trophozoite and schizont stages.
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M60186; AAA29687.1; -.
DR   InterPro; IPR001136; MSA_2.
DR   Pfam; PF00985; MSA_2; 1.
KW   Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;
KW   GPI-anchor; Merozoite.
FT   SIGNAL        1     20       POTENTIAL.
FT   CHAIN        21    238       MEROZOITE SURFACE ANTIGEN 2.
FT   PROPEP      239    262       HYDROPHOBIC, REMOVED DURING MATURATION
FT                                (BY SIMILARITY).
FT   DOMAIN        44    188       POLYMORPHIC REGION.
FT   DOMAIN        91     98       POLY-THR.
FT   CARBOHYD      22     22       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD      36     36       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     139    139       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     211    211       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     235    235       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     236    236       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   262 AA;  27374 MW;  72E0B2A315E9D154 CRC64;

  Query Match             11.9%;  Score 72.5;  DB 1;  Length 262;
  Best Local Similarity   37.5%;  Pred. No. 4.1;
  Matches   24;  Conservative    6;  Mismatches   21;  Indels   13;  Gaps    4;

Qy          39 TMGNSCICRDDSGTDDSV------DT-----QQQQAENSAVPTADTRSQPRDPVRPPRRG 87
               |  || : : || | :|       ||      | :|||||| |||:    |      |  :|
Db         137 TQNNSNV-QQDSQTKSNVPPTQDADTKSPTAQPEQAENSA-PTAEQTESPELQSAPENKG 194

Qy          88 RGPH 91
               | |
Db         195 TGQH 198


RESULT 10
MSA2_PLAP7
ID   MSA2_PLAP7     STANDARD;      PRT;   272 AA.
AC   P50498;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
DE   Merozoite surface antigen 2 precursor (MSA-2) (45 kDa merozoite
DE   surface antigen).
GN   MSA2.
OS   Plasmodium falciparum (isolate 3D7).
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=36329;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90205972; PubMed=2181307;
RA   Smythe J.A., Peterson M.G., Coppel R.L., Saul A.J., Kemp D.J.,
RA   Anders R.F.;
RT   "Structural diversity in the 45-kilodalton merozoite surface antigen
RT   of Plasmodium falciparum.";
RL   Mol. Biochem. Parasitol. 39:227-234(1990).
CC   -!- FUNCTION: May play a role in the merozoite attachment to the
CC       erythrocyte.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC       (Potential).
CC   -!- DEVELOPMENTAL STAGE: During the trophozoite and schizont stages.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M28891; AAA29686.1; -.
DR   InterPro; IPR001136; MSA_2.
DR   Pfam; PF00985; MSA_2; 1.
KW   Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;
KW   GPI-anchor; Merozoite.
FT   SIGNAL        1     20       POTENTIAL.
FT   CHAIN        21    248       MEROZOITE SURFACE ANTIGEN 2.
FT   PROPEP      249    272       HYDROPHOBIC, REMOVED DURING MATURATION
FT                                (BY SIMILARITY).
FT   DOMAIN        44    198       POLYMORPHIC REGION.
FT   DOMAIN        95    108       POLY-THR.
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FT   CARBOHYD     22     22       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     36     36       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    149    149       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    221    221       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    245    245       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    246    246       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   272 AA;  27971 MW;  9D9CF223BF2B483D CRC64;

  Query Match             11.9%;  Score 72.5;  DB 1;  Length 272;
  Best Local Similarity   37.5%;  Pred. No. 4.3;
  Matches   24;  Conservative    6;  Mismatches   21;  Indels   13;  Gaps    4;

Qy         39 TMGNSCICRDDSGTDDSV------DT-----QQQQAENSAVPTADTRSQPRDPVRPPRRG 87
              |  || : : || |  :|       ||     | :|||||| |||:    |     |  :|
Db        147 TQNNSNV-QQDSQTKSNVPPTQDADTKSPTAQPEQAENSA-PTAEQTESPELQSAPENKG 204

Qy         88 RGPH 91
              | |
Db        205 TGQH 208


RESULT 11
MSA2_PLAF6
ID   MSA2_PLAF6     STANDARD;      PRT;   274 AA.
AC   P50497;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
DE   Merozoite surface antigen 2 precursor (MSA-2).
GN   MSA2.
OS   Plasmodium falciparum (isolate kf1916).
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=57269;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92178286; PubMed=1542312;
RA   Marshall V.M., Coppel R.L., Anders R.F., Kemp D.J.;
RT   "Two novel alleles within subfamilies of the merozoite surface
RT   antigen 2 (MSA-2) of Plasmodium falciparum.";
RL   Mol. Biochem. Parasitol. 50:181-184(1992).
CC   -!- FUNCTION: May play a role in the merozoite attachment to the
CC       erythrocyte.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC       (Potential).
CC   -!- DEVELOPMENTAL STAGE: During the trophozoite and schizont stages.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M73810; AAA29698.1; -.
DR   PIR; A45632; A45632.
DR   InterPro; IPR001136; MSA_2.
DR   Pfam; PF00985; MSA_2; 1.
KW   Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;
KW   GPI-anchor; Merozoite.
FT   SIGNAL       1     20       POTENTIAL.
FT   CHAIN       21    250       MEROZOITE SURFACE ANTIGEN 2.
FT   PROPEP     251    274       HYDROPHOBIC, REMOVED DURING MATURATION
FT                               (BY SIMILARITY).
FT   DOMAIN       44    200       POLYMORPHIC REGION.
FT   DOMAIN       97    110       POLY-THR.
FT   CARBOHYD     22     22       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     36     36       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    151    151       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    223    223       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    248    248       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   274 AA;  28367 MW;  CEA832D766F743A2 CRC64;

  Query Match             11.9%;  Score 72.5;  DB 1;  Length 274;
  Best Local Similarity   37.5%;  Pred. No. 4.3;
  Matches   24;  Conservative    6;  Mismatches   21;  Indels   13;  Gaps    4;

Qy         39 TMGNSCICRDDSGTDDSV------DT-----QQQQAENSAVPTADTRSQPRDPVRPPRRG 87
              |  || : : || |  :|       ||     | :|||||| |||:    |     |  :|
Db        149 TQNNSNV-QQDSQTKSNVPPTQDADTKSPTAQPEQAENSA-PTAEQTESPELQSAPENKG 206

Qy         88 RGPH 91
              | |
Db        207 TGQH 210


RESULT 12
MSA2_PLAFG
ID   MSA2_PLAFG     STANDARD;      PRT;   287 AA.
AC   P19260;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
DE   Merozoite surface antigen 2 precursor (MSA-2) (Allelic form 2)
DE   (Membrane protein PF7).
GN   MSA2.
OS   Plasmodium falciparum (isolate FCR-3 / Gambia).
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5838;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90349616; PubMed=1696728;
RA   Elliott J.F., Albrecht G.R., Gilladoga A., Handunnetti S.M.,
RA   Neequaye J., Lallinger G., Minjas J.N., Howard R.J.;
RT   "Genes for Plasmodium falciparum surface antigens cloned by
RT   expression in COS cells.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:6363-6367(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91117264; PubMed=1990294;
RA   Fenton B., Clark J.T., Khan C.M.A., Robinson J.V., Walliker D.,
RA   Ridley R., Scaife J.G., McBride J.S.;
RT   "Structural and antigenic polymorphism of the 35- to 48-kilodalton
RT   merozoite surface antigen (MSA-2) of the malaria parasite Plasmodium
RT   falciparum.";
RL   Mol. Cell. Biol. 11:963-971(1991).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91218803; PubMed=2090943;
RA   Thomas A.W., Carr D.A., Carter J.M., Lyon J.A.;
RT   "Sequence comparison of allelic forms of the Plasmodium falciparum
RT   merozoite surface antigen MSA2.";
RL   Mol. Biochem. Parasitol. 43:211-220(1990).
CC   -!- FUNCTION: May play a role in the merozoite attachment to the
CC       erythrocyte.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC       (Potential).
CC   -!- DEVELOPMENTAL STAGE: During the trophozoite and schizont stages.
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CC   ---------------------------------------------------------------------
DR   EMBL; M28890; AAA29650.1; -.
DR   EMBL; X53832; CAA37829.1; -.
DR   EMBL; M60188; AAA29688.1; -.
DR   PIR; B39615; B39615.
DR   InterPro; IPR001136; MSA_2.
DR   Pfam; PF00985; MSA_2; 1.
KW   Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;
KW   GPI-anchor; Merozoite.
FT   SIGNAL       1     20       POTENTIAL.
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FT   CHAIN        21    263       MEROZOITE SURFACE ANTIGEN 2.
FT   PROPEP      264    287       HYDROPHOBIC, REMOVED DURING MATURATION
FT                                (BY SIMILARITY).
FT   DOMAIN       44    213       POLYMORPHIC REGION.
FT   CARBOHYD     22     22       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     36     36       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    164    164       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    236    236       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    260    260       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    261    261       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   287 AA;  28555 MW;  3968B90DAA917AF8 CRC64;

  Query Match             11.9%;  Score 72.5;  DB 1;  Length 287;
  Best Local Similarity   37.5%;  Pred. No. 4.5;
  Matches   24;  Conservative    6;  Mismatches   21;  Indels   13;  Gaps    4;

Qy         39 TMGNSCICRDDSGTDDSV------DT-----QQQQAENSAVPTADTRSQPRDPVRPPRRG 87
              |  || : : || |  :|      ||      | :|||||| |||:    |      | :|
Db        162 TQNNSNV-QQDSQTKSNVPPTQDADTKSPTAQPEQAENSA-PTAEQTESPELQSAPENKG 219

Qy         88 RGPH 91
              | |
Db        220 TGQH 223


RESULT 13
MSA2_PLAFI
ID   MSA2_PLAFI     STANDARD;      PRT;   300 AA.
AC   Q03644;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   Merozoite surface antigen 2 precursor (MSA-2).
GN   MSA2.
OS   Plasmodium falciparum (isolate imr143).
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=57268;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91156685; PubMed=2000383;
RA   Smythe J.A., Coppel R.L., Day K.P., Martin R.K., Oduola A.M.J.,
RA   Kemp D.J., Anders R.F.;
RT   "Structural diversity in the Plasmodium falciparum merozoite surface
RT   antigen 2.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:1751-1755(1991).
CC   -!- FUNCTION: May play a role in the merozoite attachment to the
CC       erythrocyte.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC       (Potential).
CC   -!- DEVELOPMENTAL STAGE: During the trophozoite and schizont stages.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M59767; AAA29695.1; -.
DR   InterPro; IPR001136; MSA_2.
DR   Pfam; PF00985; MSA_2; 1.
KW   Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;
KW   GPI-anchor; Merozoite.
FT   SIGNAL        1     20       POTENTIAL.
FT   CHAIN        21    276       MEROZOITE SURFACE ANTIGEN 2.
FT   PROPEP      277    300       HYDROPHOBIC, REMOVED DURING MATURATION
FT                                (BY SIMILARITY).
FT   DOMAIN       44    226       POLYMORPHIC REGION.
FT   DOMAIN      129    136       POLY-THR.
FT   CARBOHYD     22     22       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     36     36       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    177    177       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    249    249       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    273    273       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    274    274       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   300 AA;  30131 MW;  A01E17D36075D7D6 CRC64;

  Query Match             11.9%;  Score 72.5;  DB 1;  Length 300;
  Best Local Similarity   37.5%;  Pred. No. 4.8;
  Matches   24;  Conservative    6;  Mismatches   21;  Indels   13;  Gaps    4;

Qy         39 TMGNSCICRDDSGTDDSV------DT-----QQQQAENSAVPTADTRSQPRDPVRPPRRG 87
              |  || : : || |  :|      ||      | :|||||| |||:    |      | :|
Db        175 TQNNSNV-QQDSQTKSNVPRTQDADTKSPTAQPEQAENSA-PTAEQTESPELQSAPENKG 232

Qy         88 RGPH 91
              | |
Db        233 TGQH 236


RESULT 14
MSA2_PLAFZ
ID   MSA2_PLAFZ     STANDARD;      PRT;   300 AA.
AC   Q03645;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
DE   Merozoite surface antigen 2 precursor (MSA-2).
GN   MSA2.
OS   Plasmodium falciparum (isolate mad71 / Papua New Guinea).
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=70154;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91156685; PubMed=2000383;
RA   Smythe J.A., Coppel R.L., Day K.P., Martin R.K., Oduola A.M.J.,
RA   Kemp D.J., Anders R.F.;
RT   "Structural diversity in the Plasmodium falciparum merozoite surface
RT   antigen 2.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:1751-1755(1991).
CC   -!- FUNCTION: May play a role in the merozoite attachment to the
CC       erythrocyte.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC       (Potential).
CC   -!- DEVELOPMENTAL STAGE: During the trophozoite and schizont stages.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M59768; AAA29696.1; -.
DR   PIR; A39112; A39112.
DR   InterPro; IPR001136; MSA_2.
DR   Pfam; PF00985; MSA_2; 1.
KW   Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;
KW   GPI-anchor; Merozoite.
FT   SIGNAL        1     20       POTENTIAL.
FT   CHAIN        21    276       MEROZOITE SURFACE ANTIGEN 2.
FT   PROPEP      277    300       HYDROPHOBIC, REMOVED DURING MATURATION
FT                                (BY SIMILARITY).
FT   DOMAIN       44    226       POLYMORPHIC REGION.
FT   DOMAIN      129    136       POLY-THR.
FT   CARBOHYD     22     22       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     36     36       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    177    177       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    249    249       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    273    273       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    274    274       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   300 AA;  30101 MW;  E4116107747AA10D CRC64;

  Query Match             11.9%;  Score 72.5;  DB 1;  Length 300;
```

```
  Best Local Similarity   37.5%;  Pred. No. 4.8;
  Matches   24;  Conservative    6;  Mismatches   21;  Indels   13;  Gaps    4;

Qy         39 TMGNSCICRDDSGTDDSV------DT-----QQQQAENSAVPTADTRSQPRDPVRPPRRG 87
              |  || : : || |  :|       ||      | :|||||| |||:    |      |  :|
Db        175 TQNNSNV-QQDSQTKSNVPRTQDADTKSPTAQPEQAENSA-PTAEQTESPELQSAPENKG 232

Qy         88 RGPH 91
              | |
Db        233 TGQH 236


RESULT 15
MSA2_PLAF9
ID   MSA2_PLAF9     STANDARD;      PRT;   302 AA.
AC   Q03994;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
DE   Merozoite surface antigen 2 precursor (MSA-2).
GN   MSA2.
OS   Plasmodium falciparum (isolate tak 9).
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=57276;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91117264; PubMed=1990294;
RA   Fenton B., Clark J.T., Khan C.M.A., Robinson J.V., Walliker D.,
RA   Ridley R., Scaife J.G., McBride J.S.;
RT   "Structural and antigenic polymorphism of the 35- to 48-kilodalton
RT   merozoite surface antigen (MSA-2) of the malaria parasite Plasmodium
RT   falciparum.";
RL   Mol. Cell. Biol. 11:963-971(1991).
CC   -!- FUNCTION: May play a role in the merozoite attachment to the
CC       erythrocyte.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC       (Potential).
CC   -!- DEVELOPMENTAL STAGE: During the trophozoite and schizont stages.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X53833; CAA37830.1; -.
DR   PIR; A39615; A39615.
DR   InterPro; IPR001136; MSA_2.
DR   Pfam; PF00985; MSA_2; 1.
KW   Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;
KW   GPI-anchor; Merozoite.
FT   SIGNAL        1     20       POTENTIAL.
FT   CHAIN        21    278       MEROZOITE SURFACE ANTIGEN 2.
FT   PROPEP      279    302       HYDROPHOBIC, REMOVED DURING MATURATION
FT                                (BY SIMILARITY).
FT   DOMAIN       44    228       POLYMORPHIC REGION.
FT   DOMAIN      131    138       POLY-THR.
FT   CARBOHYD     22     22       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     36     36       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    179    179       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    251    251       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    275    275       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    276    276       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   302 AA;  30259 MW;  4E0A7EB08227CF66 CRC64;

  Query Match             11.9%;  Score 72.5;  DB 1;  Length 302;
  Best Local Similarity   37.5%;  Pred. No. 4.8;
  Matches   24;  Conservative    6;  Mismatches   21;  Indels   13;  Gaps    4;

Qy         39 TMGNSCICRDDSGTDDSV------DT-----QQQQAENSAVPTADTRSQPRDPVRPPRRG 87
              |  || : : || |  :|       ||      | :|||||| |||:    |      |  :|
Db        177 TQNNSNV-QQDSQTKSNVPRTQDADTKSPTAQPEQAENSA-PTAEQTESPELQSAPENKG 234

Qy         88 RGPH 91
              | |
Db        235 TGQH 238


Search completed: April  2, 2004, 09:53:19
Job time : 18 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 2, 2004, 09:39:06 ; Search time 21 Seconds
(without alignments)
535.924 Million cell updates/sec

Title: US-10-066-500-9
Perfect score: 609
Sequence: 1 MIVFGWAVFLASRSLGQGLL.....QNVDGLVLDTLAVIRTLVDK 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	85.5	14.0	290	2	T22161	hypothetical prote
2	79	13.0	612	2	T37181	thiamin biosynthes
3	75.5	12.4	900	2	B87957	protein Y106G6D.7
4	75.5	12.4	948	2	T26417	hypothetical prote
5	75	12.3	278	2	S39310	merozoite surface
6	75	12.3	286	2	B45632	merozoite surface
7	73.5	12.1	91	2	PL0227	T-cell receptor be
8	73	12.0	1466	1	CGHU7L	collagen alpha 1(I
9	73	12.0	2218	2	B84683	hypothetical prote
10	72.5	11.9	265	2	T05085	hypothetical prote
11	72.5	11.9	272	2	G71618	merozoite surface
12	72.5	11.9	274	2	A45632	merozoite surface
13	72.5	11.9	287	2	B39615	merozoite 45K surf
14	72.5	11.9	300	2	A39112	merozoite 45K surf
15	72.5	11.9	302	2	A39615	merozoite 45K surf
16	72.5	11.9	347	2	B39112	merozoite 45K surf
17	72.5	11.9	458	2	S24457	hypothetical prote
18	72	11.8	707	2	T26218	hypothetical prote
19	72	11.8	1787	2	T20160	hypothetical prote
20	71.5	11.7	390	2	A47312	NS34 homolog - mur
21	71	11.7	210	2	T41982	hypothetical prote
22	71	11.7	1479	2	T17401	transcription regu
23	70.5	11.6	3759	2	A35085	trithorax protein
24	70	11.5	113	2	T24164	hypothetical prote
25	69.5	11.4	279	2	T19828	hypothetical prote
26	69.5	11.4	318	2	C84651	hypothetical prote
27	69.5	11.4	773	2	F90537	lipoprotein [impor
28	69	11.3	261	2	AB3070	conserved hypothet
29	69	11.3	281	2	S26052	hypothetical prote
30	69	11.3	319	2	H98216	hypothetical prote
31	69	11.3	545	2	F84533	Mutator-like trans
32	69	11.3	775	2	B72074	hypothetical prote
33	69	11.3	775	2	C81594	hypothetical prote
34	69	11.3	775	2	D86549	hypothetical prote
35	69	11.3	876	2	PC2219	polypeptide - hepa
36	68.5	11.2	361	2	B56940	integral membrane
37	68.5	11.2	788	2	T25061	hypothetical prote
38	68	11.2	85	2	JH0786	transcription fact
39	68	11.2	180	2	B45613	surface antigen FU
40	68	11.2	208	2	T46896	merozoite surface
41	68	11.2	272	2	T29446	hypothetical prote
42	68	11.2	351	2	T51513	hypothetical prote
43	68	11.2	445	2	A56043	steroid hormone re
44	68	11.2	482	2	A70963	hypothetical prote
45	68	11.2	504	2	S75134	cell division prot

ALIGNMENTS

RESULT 1
T22161
hypothetical protein F44D12.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T22161
R;Coles, L.
submitted to the EMBL Data Library, December 1995
A;Reference number: Z19525
A;Accession: T22161
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-290 <WIL>
A;Cross-references: EMBL:Z68298; PIDN:CAA92602.1; GSPDB:GN00022; CESP:F44D12.6
A;Experimental source: clone F44D12
C;Genetics:
A;Gene: CESP:F44D12.6
A;Map position: 4
A;Introns: 19/3; 154/2; 198/3

Query Match 14.0%; Score 85.5; DB 2; Length 290;
Best Local Similarity 30.0%; Pred. No. 0.47;
Matches 27; Conservative 15; Mismatches 31; Indels 17; Gaps 5;

```
Qy          24 EEHIAHFLGTGGAATTMGN-SCICRDDSGTD-----DSVDTQQQQAENSAVPTADTRSQP 77
               : |: |:  || |     | :|  :|| | |     :| : |::   || :| :|
Db         154 DAHV-HWRETGLAFIIRSNDACRSKDDGGCDTIDSQNSKEDQERSKVNSEMPLSD----- 207

Qy          78 RDPVRPPRRGRGPHEPRRKKQNVDGLVLDT 107
               : | | |:      ||| ||   | :: |
Db         208 KKPDRKPQ-----ETPRRSKQRTPGPMMPT 232
```

RESULT 2
T37181
thiamin biosynthesis protein thiC SCQ11.11 [similarity] - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Feb-2000
C;Accession: T37181
R;Seeger, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1999
A;Reference number: Z21598
A;Accession: T37181
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-612 <SEE>
A;Cross-references: EMBL:AL096823; PIDN:CAB46966.1; GSPDB:GN00070; SCOEDB:SCQ11.11
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: thiC; SCOEDB:SCQ11.11
C;Superfamily: thiamin biosynthesis protein thiC

```
  Query Match             13.0%;  Score 79;  DB 2;  Length 612;
  Best Local Similarity   31.2%;  Pred. No. 4.6;
  Matches   30;  Conservative    7;  Mismatches   37;  Indels   22;  Gaps    4;

Qy         39 TMGNSCICRDDSG--TDDSVDTQQQQA-----ENSAVPTADTRSQPRDPVRP-------- 83
              | | |   | ||  ||  |||  ::      ||  :   ||       ||||
Db         60 TNGQSVTLYDTSGPYTDPLVDTDVRRGLAPLRENWIIARGDTEEYAGRPVRPEDDGIKHT 119

Qy         84 -PRRGRG------PHEPRRKKQNVDGLVLDTLAVIR 112
               || |         |  ||: ::  ||  :  ||  |
Db        120 SPRGGLRNLDAVFPGRPRQPRRGRDGNAVTQLAYAR 155


RESULT 3
B87957
protein Y106G6D.7 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: B87957
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: B87957
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-900 <STO>
A;Cross-references: GB:chr_I; PIDN:CAA20980.1; PID:g3880680; GSPDB:GN00019; CESP:Y106G6D
C;Genetics:
A;Gene: Y106G6D.7
A;Map position: 1

  Query Match             12.4%;  Score 75.5;  DB 2;  Length 900;
  Best Local Similarity   31.7%;  Pred. No. 16;
  Matches   20;  Conservative   10;  Mismatches   18;  Indels   15;  Gaps    2;

Qy         50 SGTDDSVDTQQQQAENSAVPTADTRSQPRDPVR-----------PPRRGRGPHEPRRKKQ 98
              |  ||   ::: : ||    |:  ||  | |:|           ||||  |    |||:::
Db        496 SHEDDDKKSRRSRWEN----TSPIRSPRRSPLRRDNRDRSRSRSPPRRRRRSRSPRRREE 551

Qy         99 NVD 101
              : |
Db        552 HTD 554


RESULT 4
T26417
hypothetical protein Y106G6D.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T26417
R;McMurray, A.
submitted to the EMBL Data Library, September 1998
A;Reference number: Z20211
A;Accession: T26417
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-948 <WIL>
A;Cross-references: EMBL:AL031629; PIDN:CAA20980.2; GSPDB:GN00019; CESP:Y106G6D.7
A;Experimental source: clone Y106G6D
C;Genetics:
A;Gene: CESP:Y106G6D.7
A;Map position: 1
A;Introns: 68/3; 160/3; 270/2; 624/2; 706/3; 888/3; 924/3

  Query Match             12.4%;  Score 75.5;  DB 2;  Length 948;
  Best Local Similarity   31.7%;  Pred. No. 16;
  Matches   20;  Conservative   10;  Mismatches   18;  Indels   15;  Gaps    2;

Qy         50 SGTDDSVDTQQQQAENSAVPTADTRSQPRDPVR-----------PPRRGRGPHEPRRKKQ 98
              |  ||   ::: : ||    |:  ||  | |:|           ||||  |    |||:::
Db        544 SHEDDDKKSRRSRWEN----TSPIRSPRRSPLRRDNRDRSRSRSPPRRRRRSRSPRRREE 599

Qy         99 NVD 101
              : |
Db        600 HTD 602


RESULT 5
S39310
merozoite surface antigen - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 17-Nov-2000
C;Accession: S39310
R;Ramasamy, R.; Ranasinghe, C.
submitted to the EMBL Data Library, November 1993
A;Description: Cycle ds DNA sequencing of a malaria parasite protein from infected blood
A;Reference number: S39310
A;Accession: S39310
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-278 <RAM>
A;Cross-references: EMBL:X76087; NID:g434996; PID:g836639
C;Superfamily: Epstein-Barr virus nuclear antigen
C;Keywords: surface antigen

  Query Match             12.3%;  Score 75;  DB 2;  Length 278;
  Best Local Similarity   34.6%;  Pred. No. 5;
  Matches   27;  Conservative    6;  Mismatches   25;  Indels   20;  Gaps    5;

Qy         32 GTGGA-------ATTMGNSCICRDDSGTDDSV------DT-----QQQQAENSAVPTADT 73
              | ||          |  || : : || |  :|       ||     | :|||||| |||:
Db        139 GNGGVQKPNQANKETQNNSNV-QQDSQTKSNVPPTQDADTKSPTAQPEQAENSA-PTAEQ 196

Qy         74 RSQPRDPVRPPRRGRGPH 91
                  |  :| | |
Db        197 TESPELQSAPENKGTGQH 214


RESULT 6
B45632
merozoite surface antigen 2 - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
C;Accession: B45632
R;Marshall, V.M.; Coppel, R.L.; Anders, R.F.; Kemp, D.J.
Mol. Biochem. Parasitol. 50, 181-184, 1992
A;Title: Two novel alleles within subfamilies of the merozoite surface antigen 2 (MSA-2)
A;Reference number: A45632; MUID:92178286; PMID:1542312
A;Accession: B45632
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-286 <MAR>
A;Experimental source: isolate 311
A;Note: sequence extracted from NCBI backbone (NCBIN:85255, NCBIP:85259)
C;Superfamily: Epstein-Barr virus nuclear antigen
C;Keywords: surface antigen

  Query Match             12.3%;  Score 75;  DB 2;  Length 286;
  Best Local Similarity   34.6%;  Pred. No. 5.1;
  Matches   27;  Conservative    6;  Mismatches   25;  Indels   20;  Gaps    5;

Qy         32 GTGGA-------ATTMGNSCICRDDSGTDDSV------DT-----QQQQAENSAVPTADT 73
              | ||          |  || : : || |  :|       ||     | :|||||| |||:
Db        147 GNGGVQKPNQANKETQNNSNV-QQDSQTKSNVPPTQDADTKSPTAQPEQAENSA-PTAEQ 204

Qy         74 RSQPRDPVRPPRRGRGPH 91
                  |     | :| | |
Db        205 TESPELQSAPENKGTGQH 222


RESULT 7
PL0227
T-cell receptor beta chain V region (V-beta-6.7a, PCR-1) - human (fragment)
```

C;Species: Homo sapiens (man)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 30-May-1997
C;Accession: PL0227
R;Li, Y.; Szabo, P.; Robinson, M.A.; Dong, B.; Posnett, D.N.
J. Exp. Med. 171, 221-230, 1990
A;Title: Allelic variations in the human T cell receptor V-beta-6.7 gene products.
A;Reference number: PL0225; MUID:90111615; PMID:1967299
A;Accession: PL0227
A;Molecule type: mRNA
A;Residues: 1-91 <LIY>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor

Query Match 12.1%; Score 73.5; DB 2; Length 91;
Best Local Similarity 34.1%; Pred. No. 2.1;
Matches 30; Conservative 8; Mismatches 21; Indels 29; Gaps 5;

```
Qy          7 AVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSG----------TDDSV 56
              |:.   :||||||     | : :|          |||    | ||          |  ||
Db         10 ALYWYRQSLGQGL-----EFLIYF---------QGNS--APDKSGLPSDRFSAERTGGSV 53

Qy         57 DT---QQQQAENSAVPTADTRSQPRDPV 81
              |   |: | |:|||    :   |||||
Db         54 STLTIQRTQQEDSAVYLCASMPVPRDPV 81
```

RESULT 8
CGHU7L
collagen alpha 1(III) chain precursor - human
N;Alternate names: procollagen alpha 1(III) chain
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 01-Sep-1995 #text_change 21-Jul-2000
C;Accession: S05272; S04642; PE0011; S01726; S04887; A90399; A94562; I51868; S59511; A9
R;Prockop, D.J.
submitted to the EMBL Data Library, February 1989
A;Reference number: S05272
A;Accession: S05272
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1240,'V',1242-1466 <PRC>
A;Cross-references: EMBL:X14420; NID:g30057; PIDN:CAA32583.1; PID:g30058
R;Ala-Kokko, L.; Kontusaari, S.; Baldwin, C.T.; Kuivaniemi, H.; Prockop, D.J.
Biochem. J. 260, 509-516, 1989
A;Title: Structure of cDNA clones coding for the entire prepro-alpha1(III) chain of huma
erences.
A;Reference number: S04642; MUID:89350838; PMID:2764886
A;Accession: S04642
A;Molecule type: mRNA
A;Residues: 1-1196 <ALA>
A;Cross-references: EMBL:X14420; NID:g30057; PIDN:CAA32583.1; PID:g30058
A;Note: the complete sequence is not shown
R;Benson-Chanda, V.; Su, M.W.; Weil, D.; Chu, M.L.; Ramirez, F.
Gene 78, 255-265, 1989
A;Title: Cloning and analysis of the 5' portion of the human type-III procollagen gene (
A;Reference number: PE0011; MUID:89378752; PMID:2777083
A;Accession: PE0011
A;Molecule type: DNA
A;Residues: 1-176 <BEN>
A;Cross-references: GB:M26939; NID:g180813; PIDN:AAA52040.1; PID:g180814
R;Toman, P.D.; Ricca, G.A.; de Crombrugghe, B.
Nucleic Acids Res. 16, 7201, 1988
A;Title: Nucleotide sequence of a cDNA coding for the amino-terminal region of human pre
A;Reference number: S01726; MUID:88303360; PMID:3405773
A;Accession: S01726
A;Molecule type: mRNA
A;Residues: 1-170 <TOM>
A;Cross-references: EMBL:X07240; NID:g30060; PIDN:CAA30229.1; PID:g30061
A;Note: the authors translated the codon CAG for residue 154 as His
R;Janeczko, R.A.; Ramirez, F.
Nucleic Acids Res. 17, 6742, 1989
A;Title: Nucleotide and amino acid sequences of the entire human alpha-1 (III) collagen.
A;Reference number: S04887; MUID:89386015; PMID:2780304
A;Accession: S04887
A;Molecule type: mRNA
A;Residues: 149-163,'G',164-240,'D',242-471,'D',473-487,'L',489,'S',491-613,'Y',615-634,
A;Cross-references: EMBL:X15332; NID:g29545; PIDN:CAA33387.1; PID:g930045
A;Note: the authors' translation of residues 905-932 is inconsistent with the nucleotide
R;Seyer, J.M.; Kang, A.H.
Biochemistry 16, 1158-1164, 1977
A;Title: Covalent structure of collagen: amino acid sequence of cyanogen bromide peptide
A;Reference number: A90399; MUID:77134724; PMID:557335
A;Accession: A90399
A;Molecule type: protein
A;Residues: 'V',169-225,229-232,'P',234-292,'D',294-398 <SEY1>
A;Experimental source: liver
A;Note: sequence corrected by A94562; attachment of 2-O-alpha-D-glucosyl-O-beta-D-galact
R;Seyer, J.M.
submitted to the Atlas, December 1977
A;Reference number: A94562
A;Accession: A94562
A;Molecule type: protein
A;Residues: 'V',169-225,229-277,'A',279-292,'D',294,'S',296-398 <SEY2>
A;Experimental source: liver
A;Note: author submitted corrections to A90399
R;Milewicz, D.M.; Witz, A.M.; Smith, A.C.; Manchester, D.K.; Waldstein, G.; Byers, P.H.
Am. J. Hum. Genet. 53, 62-70, 1993
A;Title: Parental somatic and germ-line mosaicism for a multiexon deletion with unusual
fspring.
A;Reference number: I51868; MUID:93304430; PMID:8317500
A;Accession: I51868
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 186-194 <MIL>
A;Cross-references: GB:S62925; NID:g386425; PIDN:AAD13937.1; PID:g4261637
R;Chiodo, A.A.; Sillence, D.O.; Cole, W.G.; Bateman, J.F.
Biochem. J. 311, 939-943, 1995
A;Title: Abnormal type III collagen produced by an exon-17-skipping mutation of the COL3
A;Reference number: S59511; MUID:96067614; PMID:7487954
A;Accession: S59511
A;Molecule type: mRNA
A;Residues: 302-423 <CHI>
A;Cross-references: GB:S79877; NID:g1195576; PIDN:AAB35615.1; PID:g1195577
R;Seyer, J.M.; Kang, A.H.
Biochemistry 17, 3404-3411, 1978
A;Title: Covalent structure of collagen: amino acid sequence of five consecutive CNBr pe
A;Reference number: A90414; MUID:79000343; PMID:687591
A;Accession: A90414
A;Molecule type: protein
A;Residues: 399-675,'N',677-727 <SEY3>
A;Experimental source: liver
R;Lee, B.; Vitale, E.; Superti-Furga, A.; Steinmann, B.; Ramirez, F.
J. Biol. Chem. 266, 5256-5259, 1991
A;Title: G to T transversion at position +5 of a splice donor site causes skipping of the
A;Reference number: I55349; MUID:91161621; PMID:1672129
A;Accession: I55349
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 537-605 <LEE>
A;Cross-references: GB:M59312; NID:g180815; PIDN:AAA52041.1; PID:g180816
R;Seyer, J.M.; Mainardi, C.; Kang, A.H.
Biochemistry 19, 1583-1589, 1980
A;Title: Covalent structure of collagen: amino acid sequence of alpha1 (III)-CB5 from typ
A;Reference number: A90438; MUID:80198282; PMID:6246925
A;Accession: A90438
A;Molecule type: protein
A;Residues: 728-895,'A',897-964 <SEY4>
A;Experimental source: liver
R;Cole, W.G.; Chiodo, A.A.; Lamande, S.R.; Janeczko, R.; Ramirez, F.; Dahl, H.H.M.; Chan,
J. Biol. Chem. 265, 17070-17077, 1990
A;Title: A base substitution at a splice site in the COL3A1 gene causes exon skipping and
A;Reference number: A38303; MUID:91009133; PMID:2145268
A;Accession: A38303
A;Molecule type: mRNA
A;Residues: 861-1015 <COL>
A;Cross-references: GB:J05617; GB:M55603; GB:M59227; NID:g180878; PIDN:AAB59383.1; PID:g1
A;Note: a mutant sequence with 942-977 spliced out from a patient with Ehlers-Danlos synd

R;Mankoo, B.S.; Dalgleish, R.
Nucleic Acids Res. 16, 2337, 1988
A;Title: Human pro alpha1(III) collagen: cDNA sequence for the 3' end.
A;Reference number: S02119; MUID:88189827; PMID:3357782
A;Accession: S02119
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 950-1018,'Y',1020-1183,'S',1185-1466 <MAN>
A;Cross-references: EMBL:X06700; NID:g30053; PIDN:CAA29886.1; PID:g30054
R;Seyer, J.M.; Kang, A.H.
Biochemistry 20, 2621-2627, 1981
A;Title: Covalent structure of collagen: amino acid sequence of alpha1 (III)-CB9 from ty
A;Reference number: A90446; MUID:81208139; PMID:7016180
A;Accession: A90446
A;Molecule type: protein
A;Residues: 965-979,'A',981-984,'PS',987,'QN',990-1096,'P',1098-1152,'AT',1155,'S',1157-
A;Experimental source: liver
R;Loidl, H.R.; Brinker, J.M.; May, M.; Pihlajaniemi, T.; Morrow, S.; Rosenbloom, J.; Mye
Nucleic Acids Res. 12, 9383-9394, 1984
A;Title: Molecular cloning and carboxyl-propeptide analysis of human type III procollage
A;Reference number: A93551; MUID:85087944; PMID:6096827
A;Accession: A93551
A;Molecule type: mRNA
A;Residues: 1065-1155,'P',1157-1466 <LOI>
A;Cross-references: EMBL:X01655; EMBL:X01742; NID:g29584; PIDN:CAA25821.1
R;Miskulin, M.; Dalgleish, R.; Kluve-Beckerman, B.; Rennard, S.I.; Tolstoshev, P.; Brant
Biochemistry 25, 1408-1413, 1986
A;Title: Human type III collagen gene expression is coordinately modulated with the type
A;Reference number: I52393; MUID:86187804; PMID:3754462
A;Accession: I52393
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1161-1200 <MIS>
A;Cross-references: GB:M13146; NID:g180415; PIDN:AAA52003.1; PID:g180416
R;Emanuel, B.S.; Cannizzaro, L.A.; Seyer, J.M.; Myers, J.C.
Proc. Natl. Acad. Sci. U.S.A. 82, 3385-3389, 1985
A;Title: Human alpha 1(III) and alpha 2(V) procollagen genes are located on the long arm
A;Reference number: I59025; MUID:85216505; PMID:3858826
A;Accession: I79359
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1165-1196 <EMA>
A;Cross-references: GB:M11134; NID:g180417; PIDN:AAA52004.1; PID:g180418
R;Chu, M.L.; Weil, D.; de Wet, W.; Bernard, M.; Sippola, M.; Ramirez, F.
J. Biol. Chem. 260, 4357-4363, 1985
A;Title: Isolation of cDNA and genomic clones encoding human pro-alpha1(III) collagen. P
A;Reference number: A92516; MUID:85157600; PMID:2579949
A;Accession: A92516
A;Molecule type: DNA
A;Residues: 1176-1240,'V',1242-1356,'P',1358-1466 <CHU>
A;Cross-references: GB:M10615; GB:M10793; GB:M10794; GB:M10795; GB:M10796; GB:M10797; GB
A;Experimental source: liver
A;Note: the authors translated the codon TTC for residue 1057 as Tyr; the codons given f
ation
C;Comment: Prolines and lysines at the third position of the tripeptide repeating unit (
3-hydroxylated. About 15% of the lysines are 5-hydroxylated and some are subsequently G
C;Genetics:
A;Gene: GDB:COL3A1
A;Cross-references: GDB:118729; OMIM:120180
A;Map position: 2q31-2q31
A;Introns: 27/1; 94/3; 111/3; 149/3; 176/3; 554/3; 587/3; 1175/3; 1275/1; 1337/3; 1418/3
A;Note: the list of introns is incomplete; defects in this gene can result in Ehlers-Dan
C;Complex: type III collagen is a homotrimer of monomers initially linked by disulfide b
er of their length, is formed with desmosine cross-links made from lysine and allysine r
C;Function:
A;Description: structural component of extracellular fibrous polymer that maintains inte
C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;
C;Keywords: coiled coil; Ehlers-Danlos syndrome; extracellular matrix; glycoprotein; hyd
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-153/Domain: amino-terminal propeptide #status predicted <PRO>
F;31-91/Domain: von Willebrand factor type C repeat homology <VWC>
F;154-1221/Product: collagen alpha 1(III) chain #status predicted <MAT>
F;154-167/Region: amino-terminal nonhelical telopeptide
F;168-1196/Region: helical
F;1091-1093/Region: cell attachment (R-G-D) motif
F;1197-1221/Region: carboxyl-terminal nonhelical telopeptide
F;1222-1466/Domain: carboxyl-terminal propeptide #status predicted <CPR>
F;1238-1466/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
F;24/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;153-154/Cleavage site: Pro-Gln (procollagen N-endopeptidase) #status predicted
F;154/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicte
F;161,1212/Modified site: allysine (Lys) #status predicted
F;263,284,860,977,1106/Modified site: 5-hydroxylysine (Lys) #status experimental
F;263/Binding site: carbohydrate (Lys) (covalent) #status experimental
F;584,1094/Modified site: 5-hydroxylysine (Lys) (partial) #status experimental
F;948-949/Cleavage site: Gly-Ile (collagenase) #status experimental
F;1106/Binding site: carbohydrate (Lys) (covalent) #status predicted

Query Match 12.0%; Score 73; DB 1; Length 1466;
Best Local Similarity 28.8%; Pred. No. 47;
Matches 30; Conservative 10; Mismatches 36; Indels 28; Gaps 7;

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Qy         16 GQGLLLTLEEH---IAHFLGTGGAATTMGNS-------------CICRDDSGT---DDS 55
                 |  |||  |       :|      |  : :| |             |:|  |||:   ||
Db          8 GSWLLLALLHPTIILAQQEAVEGGCSHLGQSYADRDVWKPEPCQICVC--DSGSVLCDDI 65

Qy         56 V-DTQQQQAENSAVP----TADTRSQPRDPVRPPRRGRGPHEPR 94
              : | |:    | :|     |     |  | |||  |:||  |:
Db         66 ICDDQELDCPNPEIPFGECCAVCPQPPTAPTRPP-NGQGPQGPK 108
```

RESULT 9
B84683
hypothetical protein At2g28300 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: B84683
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: B84683
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2218 <STO>
A;Cross-references: GB:AE002093; NID:g4803953; PIDN:AAD29825.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g28300
A;Map position: 2

Query Match 12.0%; Score 73; DB 2; Length 2218;
Best Local Similarity 29.9%; Pred. No. 73;
Matches 29; Conservative 17; Mismatches 19; Indels 32; Gaps 7;

```
Qy         45 ICRDDS---------GTDDSV--DTQQQQAENSA---VPTADTRS---QPRDPVRPP--- 84
                :|: :|         |:: |:  ||     |||:   :||: |::   || :||||
Db         49 LCQTESPDSPQGKGEGSERSLANDTSNIPVENSSDTLLPTSPTQAITVQPMEPVRPQSHT 108

Qy         85 --------RRGRGPHEPRRKKQNVDGLVLDTLAVIRT 113
                    :||||   |:|  : :  : |   || ||
Db        109 LKEETQPIKRGRG--RPKRTDKALTPVSLS--AVSRT 141
```

RESULT 10
T05085
hypothetical protein T6K21.170 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999
C;Accession: T05085
R;Bevan, M.; Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Bancroft, I.; Mewes,
submitted to the Protein Sequence Database, February 1998
A;Reference number: Z15397
A;Accession: T05085
A;Molecule type: DNA

```
A;Residues: 1-265 <BEV>
A;Cross-references: EMBL:AL021889
A;Experimental source: cultivar Columbia; BAC clone T6K21
C;Genetics:
A;Map position: 4
A;Introns: 37/3; 59/2; 93/3; 163/1; 192/1
A;Note: T6K21.170

  Query Match             11.9%;  Score 72.5;  DB 2;  Length 265;
  Best Local Similarity   23.5%;  Pred. No. 8.4;
  Matches   36;  Conservative   24;  Mismatches   38;  Indels   55;  Gaps    9;

Qy          2 IVFGWAVFLASR--SLGQGLLLTLEEHIAH----------FLG----------TGGAA 37
              :  |: : | ::  | | | |:| :  : |          :|             |||
Db        112 VCIGYYITLVAKDPSAG-GSLVTFQTKVVHEDYSKINTLTVYLARLKSQPPPDEEIGGAK 170

Qy         38 TTMGNS----CICRDDSGTDDSVDTQQQQAENSAVPTADTRSQPRDPV------RPPRRG 87
              | :|:|    ||    | :  ||:|::       |   : | : |: |      | :|
Db        171 TGLGSSILGTCIHPCKSVSSKSVETEEN------VKQPNERLKARNAVFYIRYRYYPNKG 224

Qy         88 RGP----HEPRRKKQNVDGLVLDTLAVIRTLVD 116
              | |    |:| |           | :|:|:  :|
Db        225 RAPKGNGHKPPR----------DRIAIIKRTMD 247


RESULT 11
G71618
merozoite surface antigen MSP-2 PFB0300c - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 17-Nov-2000
C;Accession: G71618; A44950
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.
Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID:99021743; PMID:9804551
A;Accession: G71618
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-272 <GAR>
A;Cross-references: GB:AE001385; GB:AE001362; NID:g3845143; PIDN:AAC71849.1; PID:g384514
A;Experimental source: clone 3D7
R;Smythe, J.A.; Peterson, M.G.; Coppel, R.L.; Saul, A.J.; Kemp, D.J.; Anders, R.F.
Mol. Biochem. Parasitol. 39, 227-234, 1990
A;Title: Structural diversity in the 45-kilodalton merozoite surface antigen of Plasmodi
A;Reference number: A44950; MUID:90205972; PMID:2181307
A;Accession: A44950
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-54,'T',56-272 <SMY>
A;Cross-references: GB:M28891; NID:g160458; PID:g160459
C;Genetics:
A;Gene: PFB0300c
C;Superfamily: Epstein-Barr virus nuclear antigen
C;Keywords: surface antigen

  Query Match             11.9%;  Score 72.5;  DB 2;  Length 272;
  Best Local Similarity   37.5%;  Pred. No. 8.6;
  Matches   24;  Conservative    6;  Mismatches   21;  Indels   13;  Gaps    4;

Qy         39 TMGNSCICRDDSGTDDSV------DT-----QQQQAENSAVPTADTRSQPRDPVRPPRRG 87
              |  || : : || |  :|       ||      | :|||||| |||:    |      |  :|
Db        147 TQNNSNV-QQDSQTKSNVPPTQDADTKSPTAQPEQAENSA-PTAEQTESPELQSAPENKG 204

Qy         88 RGPH 91
              | |
Db        205 TGQH 208


RESULT 12
A45632
merozoite surface antigen 2 - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
C;Accession: A45632
R;Marshall, V.M.; Coppel, R.L.; Anders, R.F.; Kemp, D.J.
Mol. Biochem. Parasitol. 50, 181-184, 1992
A;Title: Two novel alleles within subfamilies of the merozoite surface antigen 2 (MSA-2)
A;Reference number: A45632; MUID:92178286; PMID:1542312
A;Contents: KF1916
A;Accession: A45632
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-274 <MAR>
A;Cross-references: GB:M73810; NID:g160484; PID:g160485
A;Note: sequence extracted from NCBI backbone (NCBIN:85252, NCBIP:85257)
C;Superfamily: Epstein-Barr virus nuclear antigen
C;Keywords: surface antigen

  Query Match             11.9%;  Score 72.5;  DB 2;  Length 274;
  Best Local Similarity   37.5%;  Pred. No. 8.7;
  Matches   24;  Conservative    6;  Mismatches   21;  Indels   13;  Gaps    4;

Qy         39 TMGNSCICRDDSGTDDSV------DT-----QQQQAENSAVPTADTRSQPRDPVRPPRRG 87
              |  || : : || |  :|       ||      | :|||||| |||:    |      |  :|
Db        149 TQNNSNV-QQDSQTKSNVPPTQDADTKSPTAQPEQAENSA-PTAEQTESPELQSAPENKG 206

Qy         88 RGPH 91
              | |
Db        207 TGQH 210


RESULT 13
B39615
merozoite 45K surface antigen precursor - malaria parasite (Plasmodium falciparum)
N;Alternate names: membrane antigen pf7
C;Species: Plasmodium falciparum
C;Date: 13-Sep-1991 #sequence_revision 13-Sep-1991 #text_change 01-Dec-2000
C;Accession: B39615; A36018; B44950; A45613
R;Fenton, B.; Clark, J.T.; Khan, C.M.A.; Robinson, J.V.; Walliker, D.; Ridley, R.; Scaife
Mol. Cell. Biol. 11, 963-971, 1991
A;Title: Structural and antigenic polymorphism of the 35- to 48-kilodalton merozoite surf
A;Reference number: A39615; MUID:91117264; PMID:1990294
A;Accession: B39615
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-287 <FEN>
A;Cross-references: EMBL:X53833
A;Note: clone T9-94
R;Elliott, J.F.; Albrecht, G.R.; Gilladoga, A.; Handunnetti, S.M.; Neequaye, J.; Lallinge
Proc. Natl. Acad. Sci. U.S.A. 87, 6363-6367, 1990
A;Title: Genes for Plasmodium falciparum surface antigens cloned by expression in COS cel
A;Reference number: A36018; MUID:90349616; PMID:1696728
A;Accession: A36018
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-287 <ELL>
A;Cross-references: GB:M28890; NID:g160406; PID:g160407
R;Smythe, J.A.; Peterson, M.G.; Coppel, R.L.; Saul, A.J.; Kemp, D.J.; Anders, R.F.
Mol. Biochem. Parasitol. 39, 227-234, 1990
A;Title: Structural diversity in the 45-kilodalton merozoite surface antigen of Plasmodiu
A;Reference number: A44950; MUID:90205972; PMID:2181307
A;Accession: B44950
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-186,'R',188-287 <SMY>
A;Cross-references: GB:M28892; NID:g160488; PID:g160489
R;Fandeur, T.; Bonnefoy, S.; Mercereau-Puijalon, O.
Mol. Biochem. Parasitol. 47, 167-178, 1991
A;Title: In vivo and in vitro derived Palo Alto lines of Plasmodium falciparum are geneti
A;Reference number: A45613; MUID:92049549; PMID:1944415
A;Accession: A45613
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 28,'E',30-186,'R',188-230,'IH' <FAN>
A;Experimental source: Uganda Palo Alto strain, merozoite
```

```
A;Note: sequence extracted from NCBI backbone (NCBIP:65035)
C;Superfamily: Epstein-Barr virus nuclear antigen
C;Keywords: membrane protein; surface antigen

  Query Match             11.9%;  Score 72.5;  DB 2;  Length 287;
  Best Local Similarity   37.5%;  Pred. No. 9.1;
  Matches   24;  Conservative    6;  Mismatches   21;  Indels   13;  Gaps    4;

Qy          39 TMGNSCICRDDSGTDDSV------DT-----QQQQAENSAVPTADTRSQPRDPVRPPRRG 87
               |  || : : || |  :|      ||      | :|||||| |||:     |      |  :|
Db         162 TQNNSNV-QQDSQTKSNVPPTQDADTKSPTAQPEQAENSA-PTAEQTESPELQSAPENKG 219

Qy          88 RGPH 91
               | |
Db         220 TGQH 223


RESULT 14
A39112
merozoite 45K surface antigen precursor - malaria parasite (Plasmodium falciparum) (isol
C;Species: Plasmodium falciparum
C;Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 17-Nov-2000
C;Accession: A39112
R;Smythe, J.A.; Coppel, R.L.; Day, K.P.; Martin, R.K.; Oduola, A.M.J.; Kemp, D.J.; Ander
Proc. Natl. Acad. Sci. U.S.A. 88, 1751-1755, 1991
A;Title: Structural diversity in the Plasmodium falciparum merozoite surface antigen 2.
A;Reference number: A39112; MUID:91156685; PMID:2000383
A;Accession: A39112
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-300 <SMY>
A;Cross-references: GB:M59765
C;Superfamily: Epstein-Barr virus nuclear antigen
C;Keywords: surface antigen

  Query Match             11.9%;  Score 72.5;  DB 2;  Length 300;
  Best Local Similarity   37.5%;  Pred. No. 9.5;
  Matches   24;  Conservative    6;  Mismatches   21;  Indels   13;  Gaps    4;

Qy          39 TMGNSCICRDDSGTDDSV------DT-----QQQQAENSAVPTADTRSQPRDPVRPPRRG 87
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Db         175 TQNNSNV-QQDSQTKSNVPRTQDADTKSPTAQPEQAENSA-PTAEQTESPELQSAPENKG 232

Qy          88 RGPH 91
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Db         233 TGQH 236


RESULT 15
A39615
merozoite 45K surface antigen precursor (clone T9-96) - malaria parasite (Plasmodium fal
C;Species: Plasmodium falciparum
C;Date: 13-Sep-1991 #sequence_revision 13-Sep-1991 #text_change 17-Nov-2000
C;Accession: A39615; S13802
R;Fenton, B.; Clark, J.T.; Khan, C.M.A.; Robinson, J.V.; Walliker, D.; Ridley, R.; Scaif
Mol. Cell. Biol. 11, 963-971, 1991
A;Title: Structural and antigenic polymorphism of the 35- to 48-kilodalton merozoite sur
A;Reference number: A39615; MUID:91117264; PMID:1990294
A;Accession: A39615
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-302 <FEN>
A;Cross-references: EMBL:X53832
C;Superfamily: Epstein-Barr virus nuclear antigen
C;Keywords: surface antigen

  Query Match             11.9%;  Score 72.5;  DB 2;  Length 302;
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Qy          39 TMGNSCICRDDSGTDDSV------DT-----QQQQAENSAVPTADTRSQPRDPVRPPRRG 87
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Db         177 TQNNSNV-QQDSQTKSNVPRTQDADTKSPTAQPEQAENSA-PTAEQTESPELQSAPENKG 234

Qy          88 RGPH 91
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Db         235 TGQH 238


Search completed: April 2, 2004, 09:54:46
Job time : 23 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 2, 2004, 09:30:36 ; Search time 54 Seconds
(without alignments)
612.186 Million cell updates/sec

Title: US-10-066-500-9
Perfect score: 609
Sequence: 1 MIVFGWAVFLASRSLGQGLL.....QNVDGLVLDTLAVIRTLVDK 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	609	100.0	117	4	AAB31180	Aab31180 Amino aci
2	609	100.0	117	6	ABO25151	Abo25151 Novel hum
3	609	100.0	117	6	ABU67269	Abu67269 Novel hum
4	609	100.0	117	6	ABU72037	Abu72037 Novel hum
5	609	100.0	117	6	ABU67138	Abu67138 Novel hum
6	609	100.0	117	6	ABU79780	Abu79780 Human sec
7	609	100.0	117	6	ABO33583	Abo33583 Novel hum
8	609	100.0	117	6	ADA47181	Ada47181 Human sec
9	609	100.0	117	7	ABO44436	Abo44436 Human sec
10	609	100.0	117	7	ABO33460	Abo33460 Novel hum
11	609	100.0	117	7	ABO19838	Abo19838 Human sec
12	609	100.0	117	7	ADC17875	Adc17875 Human PRO
13	609	100.0	117	7	ADD10295	Add10295 Human sec
14	609	100.0	117	7	ADD11255	Add11255 Human sec
15	609	100.0	117	7	ADD70521	Add70521 Human sec
16	609	100.0	117	7	ADD39598	Add39598 Human sec
17	609	100.0	117	7	ADD70044	Add70044 Human sec
18	609	100.0	117	7	ADD37048	Add37048 Human sec
19	609	100.0	117	7	ADD38165	Add38165 Human sec
20	609	100.0	117	7	ADD39121	Add39121 Human sec
21	609	100.0	117	7	ADD38644	Add38644 Human sec
22	609	100.0	117	7	ADD40075	Add40075 Human sec
23	609	100.0	117	7	ADE50296	Ade50296 Human sec
24	609	100.0	117	7	ADE19908	Ade19908 Human sec
25	609	100.0	117	7	ADE49819	Ade49819 Human sec
26	609	100.0	117	7	ADE21377	Ade21377 Human sec
27	609	100.0	117	8	ADE41256	Ade41256 Human sec
28	609	100.0	117	8	ADE41104	Ade41104 Human sec
29	609	100.0	118	3	AAY99341	Aay99341 Human PRO
30	609	100.0	118	4	AAB66090	Aab66090 Protein o
31	609	100.0	118	5	ABB84819	Abb84819 Human PRO
32	609	100.0	118	5	ABB95425	Abb95425 Human ang
33	604	99.2	289	4	AAM25871	Aam25871 Human pro
34	604	99.2	427	2	AAY25761	Aay25761 Human sec
35	604	99.2	427	3	AAB32412	Aab32412 Human sec
36	604	99.2	436	3	AAB32411	Aab32411 Human sec
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41	79.5	13.1	5002	4	ABB63723	Abb63723 Drosophil
42	78	12.8	1527	2	AAW81172	Aaw81172 Human BAZ
43	78	12.8	1531	2	AAW81173	Aaw81173 Human BAZ
44	77	12.6	2618	4	ABG02135	Abg02135 Novel hum
45	77	12.6	2622	4	ABG06418	Abg06418 Novel hum

ALIGNMENTS

RESULT 1
AAB31180
ID AAB31180 standard; protein; 117 AA.
XX
AC AAB31180;
XX
DT 20-APR-2001 (first entry)
XX
DE Amino acid sequence of human polypeptide PRO444.
XX
KW Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO183;
KW PRO185; PRO210; PRO215; PRO217; PRO242; PRO288; PRO365; PRO1361; PRO1308;
KW PRO1183; PRO1272; PRO1419; PRO4999; PRO7170; PRO248; PRO353; PRO1318;
KW PRO1600; PRO9940; PRO533; PRO301; PRO187; PRO337; PRO1411; PRO4356;
KW PRO246; PRO265; PRO941; PRO10096; PRO6003; PRO6004; PRO350; PRO2630;
KW PRO6309; cell death; genetic disorder; transgenic animal; gene therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1. .16
FT /note= "signal peptide"
FT Modified-site 18. .24
FT /note= "N-myristoylation site"
FT Modified-site 32. .38
FT /note= "N-myristoylation site"
FT Modified-site 34. .40
FT /note= "N-myristoylation site"
FT Modified-site 35. .41
FT /note= "N-myristoylation site"
FT Modified-site 51. .57
FT /note= "N-myristoylation site"
XX
PN WO200077037-A2.
XX
PD 21-DEC-2000.
XX
PF 22-MAY-2000; 2000WO-US014042.
XX
PR 15-JUN-1999; 99US-0139695P.
PR 20-JUL-1999; 99US-0145070P.
PR 26-JUL-1999; 99US-0145698P.
PR 17-AUG-1999; 99US-0149396P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.

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PR   01-DEC-1999;   99WO-US028301.
PR   02-DEC-1999;   99WO-US028565.
PR   07-DEC-1999;   99US-0169495P.
PR   05-JAN-2000; 2000WO-US000219.
PR   18-FEB-2000; 2000WO-US004341.
PR   18-FEB-2000; 2000WO-US004342.
PR   22-FEB-2000; 2000WO-US004414.
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005841.
PR   20-MAR-2000; 2000WO-US007377.
PR   30-MAR-2000; 2000WO-US008439.
PR   15-MAY-2000; 2000WO-US013358.
PR   17-MAY-2000; 2000WO-US013705.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Botstein DA,  Desnoyers L,  Eaton DL;
PI   Ferrara N,  Fong S,  Gao W,  Gerber H,  Gerritsen ME,  Goddard A;
PI   Godowski PJ,  Gurney AL,  Kljavin IJ,  Mather JP,  Napier MA,  Pan J;
PI   Paoni NF,  Roy MA,  Stewart TA,  Tumas D,  Watanabe CK,  Williams PM;
PI   Wood WI,  Zhang Z;
XX
DR   WPI; 2001-050091/06.
DR   N-PSDB; AAC86965.
XX
PT   Isolated nucleic acid molecule encoding a PRO polypeptide which is a
PT   transmembrane polypeptide is useful for gene therapy and identification
PT   of related polypeptides.
XX
PS   Claim 12; Fig 4; 244pp; English.
XX
CC   The present sequence represents a human secreted and transmembrane
CC   polypeptide. The specification describes human polypeptides, designated
CC   PRO196, PRO444, PRO183, PRO185, PRO210, PRO215, PRO217, PRO242, PRO288,
CC   PRO365, PRO1361, PRO1308, PRO1183, PRO1272, PRO1419, PRO4999, PRO7170,
CC   PRO248, PRO353, PRO1318, PRO1600, PRO9940, PRO533, PRO301, PRO187,
CC   PRO337, PRO1411, PRO4356, PRO246, PRO265, PRO941, PRO10096, PRO6003,
CC   PRO6004, PRO350, PRO2630 and PRO6309. The biological activity of cells
CC   can be modulated with agents that bind to these polypeptides, resulting
CC   in the death of the cells. The polynucleotides encoding these
CC   polypeptides are useful in the recombinant production of the
CC   polypeptides, as a hybridisation probe to screen libraries to isolate
CC   homologous sequences, or to map the gene. They may also be used for
CC   analysing genetic disorders, and to produce transgenic animals which are
CC   useful for the development and screening of therapeutically useful
CC   reagents. The polynucleotides can also be used in gene therapy e.g. to
CC   replace a defective gene
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SQ   Sequence 117 AA;

  Query Match             100.0%;  Score 609;  DB 4;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 2e-63;
  Matches  117;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db         61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDK 117


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ID   ABO25151 standard; protein; 117 AA.
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AC   ABO25151;
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DT   05-SEP-2003  (first entry)
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XX
KW   Human; secreted and transmembrane protein; PRO; antidiabetic;
KW   ophthalmological; cytostatic; immunostimulant; gene therapy;
KW   vascular endothelial growth factor inhibitor; hypertrophy of adult heart;
KW   protein secretion disorder; pancreas disorder; diabetes;
KW   vascular permeability; retinal neuron cell survival; retinal disorder;
KW   immune response; inflammation; mononuclear cell infiltration;
KW   eosinophil infiltration; apoptosis; neoplastic growth.
XX
OS   Homo sapiens.
XX
PN   US2003040014-A1.
XX
PD   27-FEB-2003.
XX
PF   01-FEB-2002; 2002US-00066269.
XX
PR   26-AUG-1997;   97US-0056974P.
PR   17-SEP-1997;   97US-0059115P.
PR   18-SEP-1997;   97US-0059263P.
PR   19-SEP-1997;   97US-0059588P.
PR   17-OCT-1997;   97US-0062285P.
PR   24-OCT-1997;   97US-0062816P.
PR   24-OCT-1997;   97US-0063082P.
PR   27-OCT-1997;   97US-0063329P.
PR   29-OCT-1997;   97US-0063733P.
PR   21-NOV-1997;   97US-0066364P.
PR   25-NOV-1997;   97US-0066840P.
PR   16-DEC-1997;   97US-0069694P.
PR   09-FEB-1998;   98US-0074086P.
PR   09-FEB-1998;   98US-0074092P.
PR   25-MAR-1998;   98US-0079294P.
PR   08-APR-1998;   98US-0081049P.
PR   14-JUL-1998;   98WO-US014552.
PR   10-AUG-1998;   98US-0095998P.
PR   18-AUG-1998;   98US-0097000P.
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PR   28-OCT-1998;   98US-0106032P.
PR   20-NOV-1998;   98US-0109304P.
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PR   25-NOV-1998;   98WO-US025190.
PR   01-DEC-1998;   98WO-US025108.
PR   08-MAR-1999;   99WO-US005028.
PR   23-MAR-1999;   99US-0125778P.
PR   02-JUN-1999;   99WO-US012252.
PR   15-JUN-1999;   99US-0139695P.
PR   20-JUL-1999;   99US-0145070P.
PR   26-JUL-1999;   99US-0145698P.
PR   17-AUG-1999;   99US-0149396P.
PR   01-SEP-1999;   99WO-US020111.
PR   08-SEP-1999;   99WO-US020594.
PR   15-SEP-1999;   99WO-US021090.
PR   15-SEP-1999;   99WO-US021547.
PR   30-NOV-1999;   99WO-US028313.
PR   01-DEC-1999;   99WO-US028301.
PR   02-DEC-1999;   99WO-US028565.
PR   07-DEC-1999;   99US-0169495P.
PR   20-DEC-1999;   99WO-US030999.
PR   05-JAN-2000; 2000WO-US000219.
PR   18-FEB-2000; 2000WO-US004341.
PR   18-FEB-2000; 2000WO-US004342.
PR   22-FEB-2000; 2000WO-US004414.
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005841.
PR   09-MAR-2000; 2000WO-US006471.
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PR   20-MAR-2000; 2000WO-US007377.
PR   30-MAR-2000; 2000WO-US008439.
PR   15-MAY-2000; 2000WO-US013358.
PR   17-MAY-2000; 2000WO-US013705.
PR   22-MAY-2000; 2000WO-US014042.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US015264.
PR   11-AUG-2000; 2000WO-US022031.
PR   23-AUG-2000; 2000WO-US023522.
PR   24-AUG-2000; 2000WO-US023328.
PR   01-DEC-2000; 2000WO-US032678.
PR   28-FEB-2001; 2001WO-US006520.
PR   30-MAY-2001; 2001WO-US017443.
PR   01-JUN-2001; 2001WO-US017800.
PR   20-JUN-2001; 2001WO-US019692.
PR   29-JUN-2001; 2001WO-US021066.
PR   09-JUL-2001; 2001WO-US021735.
PR   15-NOV-2001; 2001US-00002796.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
PI   Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI   Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
PI   Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
PI   Wood WI, Zhang Z;
XX
DR   WPI; 2003-503396/47.
DR   N-PSDB; ACD42316.
XX
PT   New secreted and transmembrane PRO polypeptides, useful for treating
PT   diabetes, retinal disorders and stimulating an immune response.
XX
PS   Claim 12; Fig 4; 254pp; English.
XX
CC   The invention describes an isolated polypeptide (I) having at least 80 %
CC   amino acid sequence identity to 30 secreted and transmembrane
CC   polypeptides. PRO polypeptides are also useful for stimulating
CC   hypertrophy of adult heart, for inhibiting vascular endothelial growth
CC   factor stimulated proliferation of endothelial cells, stimulating
CC   proliferation of stimulated T-lymphocytes and for inducing proliferation
CC   of PDB12 pancreatic ductal cells and are thus useful in the treatment of
CC   disorders which involve protein secretion by the pancreas, including
CC   diabetes. PRO polypeptides are useful for inducing vascular permeability
CC   and in enhancing survival of retinal neurons cells and are thus useful
CC   for the treatment of retinal disorders. PRO polypeptides are also useful
CC   for stimulating an immune response and inducing inflammation by inducing
CC   mononuclear cell and eosinophil infiltration at the site of infection of
CC   an animal. The PRO polypeptides are further useful for inducing apoptosis
CC   in endothelial cells for inhibiting neoplastic growth. This is the amino
CC   acid sequence of a novel human secreted and transmembrane PRO polypeptide
XX
SQ   Sequence 117 AA;

  Query Match             100.0%;  Score 609;  DB 6;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 2e-63;
  Matches  117;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQ 60

Qy         61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDK 117
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RESULT 3
ABU67269
ID   ABU67269 standard; protein; 117 AA.
XX
AC   ABU67269;
XX
DT   28-MAY-2003  (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO444.
XX
KW   Secreted and transmembrane polypeptide; PRO polypeptide; PRO533; PRO301;
KW   PRO187; PRO337; PRO1411; PRO10096; PRO246; PRO6307; PRO6003; PRO6004;
KW   PRO4356; PRO2630; PRO265; PRO941; FGFR; bioactive molecule;
KW   fibroblast growth factor receptor; cell death; chromosome mapping;
KW   gene mapping; transgenic animal; knockout animal; gene therapy; tumour;
KW   obesity; diabetes; insulinaemia; vascular permeability;
KW   cardiac insufficiency disorder; immune response; hearing loss;
KW   auditory hair cell regeneration; bone disorder; cartilage disorder;
KW   sports injury; arthritis.
XX
OS   Homo sapiens.
XX
PN   US2003032063-A1.
XX
PD   13-FEB-2003.
XX
PF   01-FEB-2002; 2002US-00066494.
XX
PR   26-AUG-1997;   97US-0056974P.
PR   17-SEP-1997;   97US-0059115P.
PR   18-SEP-1997;   97US-0059263P.
PR   19-SEP-1997;   97US-0059588P.
PR   17-OCT-1997;   97US-0062285P.
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PR   27-OCT-1997;   97US-0063329P.
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PR   09-FEB-1998;   98US-0074086P.
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PR   17-SEP-1998;   98WO-US019437.
PR   24-SEP-1998;   98US-0101922P.
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PR   20-NOV-1998;   98US-0109304P.
PR   20-NOV-1998;   98WO-US024855.
PR   25-NOV-1998;   98WO-US025190.
PR   01-DEC-1998;   98WO-US025108.
PR   08-MAR-1999;   99WO-US005028.
PR   23-MAR-1999;   99US-0125778P.
PR   02-JUN-1999;   99WO-US012252.
PR   15-JUN-1999;   99US-0139695P.
PR   20-JUL-1999;   99US-0145070P.
PR   26-JUL-1999;   99US-0145698P.
PR   17-AUG-1999;   99US-0149396P.
PR   01-SEP-1999;   99WO-US020111.
PR   08-SEP-1999;   99WO-US020594.
PR   15-SEP-1999;   99WO-US021090.
PR   15-SEP-1999;   99WO-US021547.
PR   30-NOV-1999;   99WO-US028313.
PR   01-DEC-1999;   99WO-US028301.
PR   02-DEC-1999;   99WO-US028565.
PR   07-DEC-1999;   99US-0169495P.
PR   20-DEC-1999;   99WO-US030999.
PR   05-JAN-2000; 2000WO-US000219.
PR   18-FEB-2000; 2000WO-US004341.
PR   18-FEB-2000; 2000WO-US004342.
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PR   22-FEB-2000; 2000WO-US004414.
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005841.
PR   09-MAR-2000; 2000WO-US006471.
PR   20-MAR-2000; 2000WO-US007377.
PR   30-MAR-2000; 2000WO-US008439.
PR   15-MAY-2000; 2000WO-US013358.
PR   17-MAY-2000; 2000WO-US013705.
PR   22-MAY-2000; 2000WO-US014042.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US015264.
PR   11-AUG-2000; 2000WO-US022031.
PR   23-AUG-2000; 2000WO-US023522.
PR   24-AUG-2000; 2000WO-US023328.
PR   01-DEC-2000; 2000WO-US032678.
PR   28-FEB-2001; 2001WO-US006520.
PR   30-MAY-2001; 2001WO-US017443.
PR   01-JUN-2001; 2001WO-US017800.
PR   20-JUN-2001; 2001WO-US019692.
PR   29-JUN-2001; 2001WO-US021066.
PR   09-JUL-2001; 2001WO-US021735.
PR   15-NOV-2001; 2001US-00002796.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Botstein DA,  Desnoyers L,  Eaton DL;
PI   Ferrara N,  Fong S,  Gao W,  Gerber H,  Gerritsen ME,  Goddard A;
PI   Godowski PJ,  Gurney AL,  Kljavin IJ,  Mather JP,  Napier MA,  Pan J;
PI   Paoni NF,  Roy MA,  Stewart TA,  Tumas D,  Watanabe CK,  Williams PM;
PI   Wood WI,  Zhang Z;
XX
DR   WPI; 2003-341964/32.
DR   N-PSDB; ACA04925.
XX
PT   Thirty seven nucleic acids encoding novel secreted and transmembrane PRO
PT   polypeptides, useful for modulating biological activity of cell
PT   expressing the polypeptide, and in chromosome and gene mapping.
XX
PS   Claim 12; Fig 4; 255pp; English.
XX
CC   The invention describes an isolated, secreted and transmembrane
CC   polypeptide (I), termed PRO polypeptide. (I) Is useful for detecting
CC   PRO533, PRO301, PRO187, PRO337, PRO1411, PRO10096, PRO246, PRO6307,
CC   PRO6003, PRO6004, PRO4356, PRO2630, PRO265, PRO941, fibroblast growth
CC   factor receptor (FGFR)-4, FGFR-3, FGFR-2 or FGFR-1 polypeptide, and for
CC   linking a bioactive molecule e.g. toxin, radiolabel or antibody, to a
CC   cell expressing the polypeptides. The bioactive molecule causes cell
CC   death. (II) Is useful as hybridisation probes, in chromosome and gene
CC   mapping, in generation of antisense RNA and DNA, in the preparation of
CC   PRO polypeptide, for generating transgenic animals or knockout animals
CC   which in turn are useful in the development and screening of
CC   therapeutically useful reagents, and for the genetic analysis of
CC   individuals with genetic disorders, in gene therapy, and for chromosome
CC   identification. (I) Or Ab is useful for the preparation of medicament for
CC   treating conditions which are responsive to the PRO polypeptide or anti-
CC   PRO antibody e.g. a tumour. (I) is useful for treating obesity, diabetes
CC   or hypo- or hyper-insulinaemia, and cardiac insufficiency disorders, for
CC   inhibiting tumour growth, enhances vascular permeability and immune
CC   response, for inducing regeneration of auditory hair cells and for
CC   treating hearing loss in mammals, and for treating bone and/or cartilage
CC   disorders such as sports injuries and arthritis. This is the amino acid
CC   sequence of a novel human secreted and transmembrane polypeptide
CC   associated oligonucleotide
XX
SQ   Sequence 117 AA;

  Query Match             100.0%;  Score 609;  DB 6;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 2e-63;
  Matches  117;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQ 60

Qy         61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDK 117
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDK 117


RESULT 4
ABU72037
ID   ABU72037 standard; protein; 117 AA.
XX
AC   ABU72037;
XX
DT   11-JUN-2003  (first entry).
XX
DE   Novel human secreted and transmembrane protein PRO444.
XX
KW   Human; secreted and transmembrane polypeptide; PRO;
KW   fibroblast growth factor receptor; PRO533; PRO301; PRO187; PRO337;
KW   PRO1411; PRO10096; PRO246; PRO6307; PRO6003; FGFR-3; FGFR-4; FGFR-1;
KW   FGFR-2; PRO6004; PRO4356; PRO2630; PRO265; PRO951; bioactive molecule;
KW   toxin; radiolabel; antibody; cell death; chromosome mapping;
KW   gene mapping; transgenic animal; knockout animal; gene therapy;
KW   tissue typing.
XX
OS   Homo sapiens.
XX
PN   US2002177165-A1.
XX
PD   28-NOV-2002.
XX
PF   01-FEB-2002; 2002US-00066500.
XX
PR   26-AUG-1997;   97US-0056974P.
PR   17-SEP-1997;   97US-0059115P.
PR   18-SEP-1997;   97US-0059263P.
PR   19-SEP-1997;   97US-0059588P.
PR   17-OCT-1997;   97US-0062285P.
PR   24-OCT-1997;   97US-0062816P.
PR   24-OCT-1997;   97US-0063082P.
PR   27-OCT-1997;   97US-0063329P.
PR   29-OCT-1997;   97US-0063733P.
PR   21-NOV-1997;   97US-0066364P.
PR   25-NOV-1997;   97US-0066840P.
PR   16-DEC-1997;   97US-0069694P.
PR   09-FEB-1998;   98US-0074086P.
PR   09-FEB-1998;   98US-0074092P.
PR   25-MAR-1998;   98US-0079294P.
PR   08-APR-1998;   98US-0081049P.
PR   14-JUL-1998;   98WO-US014552.
PR   10-AUG-1998;   98US-0095998P.
PR   18-AUG-1998;   98US-0097000P.
PR   09-SEP-1998;   98US-0099601P.
PR   10-SEP-1998;   98US-0099803P.
PR   10-SEP-1998;   98US-0099811P.
PR   10-SEP-1998;   98US-0099812P.
PR   10-SEP-1998;   98WO-US018824.
PR   14-SEP-1998;   98WO-US019093.
PR   16-SEP-1998;   98WO-US019330.
PR   17-SEP-1998;   98US-0100858P.
PR   17-SEP-1998;   98WO-US019437.
PR   24-SEP-1998;   98US-0101922P.
PR   28-OCT-1998;   98US-0106032P.
PR   20-NOV-1998;   98US-0109304P.
PR   20-NOV-1998;   98WO-US024855.
PR   25-NOV-1998;   98WO-US025190.
PR   01-DEC-1998;   98WO-US025108.
PR   08-MAR-1999;   99WO-US005028.
PR   23-MAR-1999;   99US-0125778P.
PR   02-JUN-1999;   99WO-US012252.
PR   15-JUN-1999;   99US-0139695P.
PR   20-JUL-1999;   99US-0145070P.
PR   26-JUL-1999;   99US-0145698P.
PR   17-AUG-1999;   99US-0149396P.
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PR   01-SEP-1999;   99WO-US020111.
PR   08-SEP-1999;   99WO-US020594.
PR   15-SEP-1999;   99WO-US021090.
PR   15-SEP-1999;   99WO-US021547.
PR   30-NOV-1999;   99WO-US028313.
PR   01-DEC-1999;   99WO-US028301.
PR   02-DEC-1999;   99WO-US028565.
PR   07-DEC-1999;   99US-0169495P.
PR   20-DEC-1999;   99WO-US030999.
PR   05-JAN-2000; 2000WO-US000219.
PR   18-FEB-2000; 2000WO-US004341.
PR   18-FEB-2000; 2000WO-US004342.
PR   22-FEB-2000; 2000WO-US004414.
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005841.
PR   09-MAR-2000; 2000WO-US006471.
PR   20-MAR-2000; 2000WO-US007377.
PR   30-MAR-2000; 2000WO-US008439.
PR   15-MAY-2000; 2000WO-US013358.
PR   17-MAY-2000; 2000WO-US013705.
PR   22-MAY-2000; 2000WO-US014042.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US015264.
PR   11-AUG-2000; 2000WO-US022031.
PR   23-AUG-2000; 2000WO-US023522.
PR   24-AUG-2000; 2000WO-US023328.
PR   01-DEC-2000; 2000WO-US032678.
PR   28-FEB-2001; 2001WO-US006520.
PR   30-MAY-2001; 2001WO-US017443.
PR   01-JUN-2001; 2001WO-US017800.
PR   20-JUN-2001; 2001WO-US019692.
PR   29-JUN-2001; 2001WO-US021066.
PR   09-JUL-2001; 2001WO-US021735.
PR   15-NOV-2001; 2001US-00002796.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Botstein DA,  Desnoyers L,  Eaton DL;
PI   Ferrara N,  Fong S,  Gao W,  Gerber H,  Gerritsen ME,  Goddard A;
PI   Godowski PJ,  Gurney AL,  Kljavin IJ,  Mather JP,  Napier MA,  Pan J;
PI   Paoni NF,  Roy MA,  Stewart TA,  Tumas D,  Watanabe CK,  Williams PM;
PI   Wood WI,  Zhang Z;
XX
DR   WPI; 2003-328482/31.
DR   N-PSDB; ACA60455.
XX
PT   Novel secreted and transmembrane polypeptide for modulating biological
PT   activity of cell expressing the polypeptide, for identifying agonists or
PT   antagonists of polypeptide, and as molecular weight markers.
XX
PS   Claim 12; Fig 4; 254pp; English.
XX
CC   The invention describes an isolated, secreted and transmembrane
CC   polypeptide (PP), termed PRO PP or fibroblast growth factor receptor PP
CC   (I). (I) is useful for detecting PRO533, PRO301, PRO187, PRO337, PRO1411,
CC   PRO10096, PRO246, PRO6307, PRO6003, fibroblast growth factor receptor
CC   (FGFR)-3, FGFR-4, FGFR-1, FGFR-2, PRO6004, PRO4356, PRO2630, PRO265 or
CC   PRO951 polypeptide, and for linking a bioactive molecule to a cell
CC   expressing the above polypeptides. The bioactive molecule, a toxin,
CC   radiolabel or an antibody, causes cell death. PRO is useful in assays to
CC   identify other proteins or molecules involved in binding interaction. The
CC   polynucleotide (II) encoding (I) is useful in chromosome and gene
CC   mapping, in generation of antisense RNA and DNA, for generating
CC   transgenic animals or knockout animals which in turn are useful in the
CC   development and screening of therapeutically useful reagents, to
CC   construct hybridisation probes for mapping the gene which encodes the PRO
CC   and for the genetic analysis of individuals with genetic disorders, in
CC   gene therapy, for chromosome identification and as a chromosome marker.
CC   (I) and (II) are useful for tissue typing. This is the amino acid
CC   sequence of a novel human secreted and transmembrane PRO polypeptide
XX
SQ   Sequence 117 AA;
```

```
  Query Match             100.0%;  Score 609;  DB 6;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 2e-63;
  Matches  117;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQ 60

Qy         61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDK 117
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDK 117
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RESULT 5
ABU67138
ID   ABU67138 standard; protein; 117 AA.
XX
AC   ABU67138;
XX
DT   28-MAY-2003  (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO444.
XX
KW   Secreted and transmembrane polypeptide; PRO polypeptide; PRO533; PRO301;
KW   PRO187; PRO337; PRO1411; PRO10096; PRO246; PRO6307; PRO6003; PRO6004;
KW   PRO4356; PRO2630; PRO265; PRO941; FGFR; bioactive molecule;
KW   fibroblast growth factor receptor; cell death; chromosome mapping;
KW   gene mapping; transgenic animal; knockout animal; gene therapy; tumour;
KW   obesity; diabetes; insulinaemia; vascular permeability;
KW   cardiac insufficiency disorder; immune response; hearing loss;
KW   auditory hair cell regeneration; bone disorder; cartilage disorder;
KW   sports injury; arthritis.
XX
OS   Homo sapiens.
XX
PN   US2003032062-A1.
XX
PD   13-FEB-2003.
XX
PF   01-FEB-2002; 2002US-00066273.
XX
PR   26-AUG-1997;   97US-0056974P.
PR   17-SEP-1997;   97US-0059115P.
PR   18-SEP-1997;   97US-0059263P.
PR   19-SEP-1997;   97US-0059588P.
PR   17-OCT-1997;   97US-0062285P.
PR   24-OCT-1997;   97US-0062816P.
PR   24-OCT-1997;   97US-0063082P.
PR   27-OCT-1997;   97US-0063329P.
PR   29-OCT-1997;   97US-0063733P.
PR   21-NOV-1997;   97US-0066364P.
PR   25-NOV-1997;   97US-0066840P.
PR   16-DEC-1997;   97US-0069694P.
PR   09-FEB-1998;   98US-0074086P.
PR   09-FEB-1998;   98US-0074092P.
PR   25-MAR-1998;   98US-0079294P.
PR   08-APR-1998;   98US-0081049P.
PR   14-JUL-1998;   98WO-US014552.
PR   10-AUG-1998;   98US-0095998P.
PR   18-AUG-1998;   98US-0097000P.
PR   09-SEP-1998;   98US-0099601P.
PR   10-SEP-1998;   98US-0099803P.
PR   10-SEP-1998;   98US-0099811P.
PR   10-SEP-1998;   98US-0099812P.
PR   10-SEP-1998;   98WO-US018824.
PR   14-SEP-1998;   98WO-US019093.
PR   16-SEP-1998;   98WO-US019330.
PR   17-SEP-1998;   98US-0100858P.
PR   17-SEP-1998;   98WO-US019437.
PR   24-SEP-1998;   98US-0101922P.
PR   28-OCT-1998;   98US-0106032P.
PR   20-NOV-1998;   98US-0109304P.
PR   20-NOV-1998;   98WO-US024855.
```

PR 25-NOV-1998; 98WO-US025190.
PR 01-DEC-1998; 98WO-US025108.
PR 08-MAR-1999; 99WO-US005028.
PR 23-MAR-1999; 99US-0125778P.
PR 02-JUN-1999; 99WO-US012252.
PR 15-JUN-1999; 99US-0139695P.
PR 20-JUL-1999; 99US-0145070P.
PR 26-JUL-1999; 99US-0145698P.
PR 17-AUG-1999; 99US-0149396P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028565.
PR 07-DEC-1999; 99US-0169495P.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 09-MAR-2000; 2000WO-US006471.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 15-NOV-2001; 2001US-00002796.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
PI Wood WI, Zhang Z;
XX
DR WPI; 2003-341963/32.
DR N-PSDB; ACA04445.
XX
PT New secreted and transmembrane polypeptide for modulating biological
PT activity of a cell expressing the polypeptide, identifying agonists or
PT antagonists of the polypeptide, and as molecular weight markers.
XX
PS Claim 12; Fig 4; 254pp; English.
XX
CC The invention describes an isolated, secreted and transmembrane
CC polypeptide (I), termed PRO polypeptide. (I) Is useful for detecting
CC PRO533, PRO301, PRO187, PRO337, PRO1411, PRO10096, PRO246, PRO6307,
CC PRO6003, PRO6004, PRO4356, PRO2630, PRO265, PRO941, fibroblast growth
CC factor receptor (FGFR)-4, FGFR-3, FGFR-2 or FGFR-1 polypeptide, and for
CC linking a bioactive molecule e.g. toxin, radiolabel or antibody, to a
CC cell expressing the polypeptides. The bioactive molecule causes cell
CC death. (II) Is useful as hybridisation probes, in chromosome and gene
CC mapping, in generation of antisense RNA and DNA, in the preparation of
CC PRO polypeptide, for generating transgenic animals or knockout animals
CC which in turn are useful in the development and screening of
CC therapeutically useful reagents, and for the genetic analysis of
CC individuals with genetic disorders, in gene therapy, and for chromosome
CC identification. (I) Or Ab is useful for the preparation of medicament for
CC treating conditions which are responsive to the PRO polypeptide or anti-
CC PRO antibody e.g. a tumour. (I) is useful for treating obesity, diabetes
CC or hypo- or hyper-insulinaemia, and cardiac insufficiency disorders, for
CC inhibiting tumour growth, enhances vascular permeability and immune
CC response, for inducing regeneration of auditory hair cells and for
CC treating hearing loss in mammals, and for treating bone and/or cartilage
CC disorders such as sports injuries and arthritis. This is the amino acid
CC sequence of a novel human secreted and transmembrane polypeptide
XX
SQ Sequence 117 AA;

Query Match 100.0%; Score 609; DB 6; Length 117;
Best Local Similarity 100.0%; Pred. No. 2e-63;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQ 60
Db 1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQ 60

Qy 61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDK 117
Db 61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDK 117

RESULT 6
ABU79780
ID ABU79780 standard; protein; 117 AA.
XX
AC ABU79780;
XX
DT 19-JUN-2003 (first entry)
XX
DE Human secreted/transmembrane protein PRO444.
XX
KW Human; secreted protein; transmembrane protein; PRO; genetic disorder;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN US2003032057-A1.
XX
PD 13-FEB-2003.
XX
PF 15-NOV-2001; 2001US-00002796.
XX
PR 26-AUG-1997; 97US-0056974P.
PR 17-SEP-1997; 97US-0059115P.
PR 18-SEP-1997; 97US-0059263P.
PR 19-SEP-1997; 97US-0059588P.
PR 17-OCT-1997; 97US-0062285P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063082P.
PR 27-OCT-1997; 97US-0063329P.
PR 29-OCT-1997; 97US-0063733P.
PR 21-NOV-1997; 97US-0066364P.
PR 25-NOV-1997; 97US-0066840P.
PR 16-DEC-1997; 97US-0069694P.
PR 09-FEB-1998; 98US-0074086P.
PR 09-FEB-1998; 98US-0074092P.
PR 25-MAR-1998; 98US-0079294P.
PR 08-APR-1998; 98US-0081049P.
PR 14-JUL-1998; 98WO-US014552.
PR 10-AUG-1998; 98US-0095998P.
PR 18-AUG-1998; 98US-0097000P.
PR 09-SEP-1998; 98US-0099601P.
PR 10-SEP-1998; 98US-0099803P.
PR 10-SEP-1998; 98US-0099811P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 16-SEP-1998; 98WO-US019330.

PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 24-SEP-1998; 98US-0101922P.
PR 28-OCT-1998; 98US-0106032P.
PR 20-NOV-1998; 98US-0109304P.
PR 20-NOV-1998; 98WO-US024855.
PR 25-NOV-1998; 98WO-US025190.
PR 01-DEC-1998; 98WO-US025108.
PR 08-MAR-1999; 99WO-US005028.
PR 23-MAR-1999; 99US-0125778P.
PR 02-JUN-1999; 99WO-US012252.
PR 15-JUN-1999; 99US-0139695P.
PR 20-JUL-1999; 99US-0145070P.
PR 26-JUL-1999; 99US-0145698P.
PR 17-AUG-1999; 99US-0149396P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028565.
PR 07-DEC-1999; 99US-0169495P.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 09-MAR-2000; 2000WO-US006471.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
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PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
XX
PA (GETH) GENENTECH INC.
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PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
PI Wood WI, Zhang Z;
XX
DR WPI; 2003-341960/32.
DR N-PSDB; ACA65586.
XX
PT Novel secreted and transmembrane polypeptide for modulating biological
PT activity of cell expressing the polypeptide, identifying agonists or
PT antagonists of polypeptide, and as molecular weight markers.
XX
PS Claim 12; Fig 4; 255pp; English.
XX
CC The invention relates to an isolated, secreted/transmembrane polypeptide,
CC termed PRO polypeptide, having at least 80% sequence identity to a
CC sequence selected from any one of the 37 sequences appearing as ABU79779
CC -ABU79815 or to a sequence encoded by a nucleic acid molecule deposited
CC under any one of the ATCC numbers given in the specification. Also
CC included are an isolated nucleic acid molecule having at least 80%
CC sequence identity to a sequence selected from any one of the 37 cDNA
CC sequences defined in the specification (or encoding the mature PRO
CC protein or a PRO protein extracellular domain), a PRO expression vector,
CC a hoist cell comprising the vector, PRO fusion proteins, anti-PRO
CC antibodies and a method for linking a bioactive molecule to a cell
CC expressing the above PRO polypeptides, the bioactive molecule is a toxin,
CC radiolabel or an antibody and causes the death of the cell. PRO or the
CC antibody is useful for modulating at least one biological activity of
CC cell expressing the above polypeptides. PRO is useful for identifying
CC agonists or antagonists of PRO, for preparing a variant of PRO, as
CC molecular weight markers for protein electrophoresis purpose and PRO
CC nucleic acid is useful for recombinantly expressing those markers. PRO is
CC also useful as therapeutic agent. PRO is useful in assays to identify
CC other proteins or molecules involved in binding interaction. PRO nucleic
CC acid is useful as hybridisation probes, in chromosome and gene mapping,
CC in generation of antisense RNA and DNA, in the preparation of PRO
CC polypeptide, in gene therapy, for generating transgenic animals or
CC knockout animals which in turn are useful in the development and
CC screening of therapeutically useful reagents, to construct hybridisation
CC probes for mapping the gene which encodes the PRO and for the genetic
CC analysis of individuals with genetic disorders, for chromosome
CC identification, as a chromosome marker, and for generating probes for
CC polymerase chain reaction (PCR), Northern analysis, Southern analysis and
CC Western analysis. The antibody is useful in diagnostic assays for PRO,
CC e.g. detecting its expression in specific cells, tissues or serum, for
CC affinity purification of PRO from recombinant cell culture or natural
CC sources. PRO or Ab is useful for the preparation of medicament for
CC treating conditions which is responsive to the PRO polypeptide or anti-
CC PRO antibody. PRO and PRO nucleic acid are useful for tissue typing. The
CC present sequence encodes a PRO polypeptide
XX
SQ Sequence 117 AA;

Query Match 100.0%; Score 609; DB 6; Length 117;
Best Local Similarity 100.0%; Pred. No. 2e-63;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQ 60

Qy         61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDK 117
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDK 117
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RESULT 7
ABO33583
ID ABO33583 standard; protein; 117 AA.
XX
AC ABO33583;
XX
DT 17-SEP-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO444.
XX
KW Human; secreted and transmembrane protein; PRO; angiogenesis;
KW endothelial cell proliferation; wound healing; immune response;
KW T-lymphocytes proliferation; neonatal heart hypertrophy; tumour;
KW cardiac insufficiency disorder; calcium flux; inflammation;
KW vascular endothelial growth factor-stimulated proliferation;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW nephropathy; Schanlein-Henoch purpura; celiac disease; Crohn's disease;
KW dermatitis herpetiformis; diabetes; haemoglobin switch; insulinaemia;
KW pancreatic beta-cell precursor cell differentiation; thalassemias;
KW obesity; auditory hair cell regeneration; hearing loss; bone disorder;
KW cartilage disorder; sports injury; arthritis.
XX
OS Homo sapiens.
XX
PN US2003073130-A1.
XX
PD 17-APR-2003.
XX

PF 11-DEC-2001; 2001US-00015869.
XX
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
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PR 01-SEP-1998; 98US-0098750P.
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PR 20-JUL-1999; 99US-0144758P.
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PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021194.
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PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
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PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.

PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX
DR WPI; 2003-585293/55.
DR N-PSDB; ACD68242.
XX
PT Novel isolated PRO polypeptides e.g. PRO1130, PRO1275, PRO1418, PRO1555,
PT PRO1787 that modulate glucose or free fatty acid uptake by skeletal
PT muscle cells, and are useful for treating diabetes, hyper- or hypo-

Query Match 100.0%; Score 609; DB 6; Length 117;
Best Local Similarity 100.0%; Pred. No. 2e-63;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQ 60

Qy 61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDK 117
Db 61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDK 117

RESULT 8
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ID ADA47181 standard; protein; 117 AA.
XX
AC ADA47181;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human secreted/transmembrane polypeptide PRO444.
XX
KW human; secreted protein; transmembrane protein; PRO; VEGF inhibitor;
KW vascular endothelial growth factor; endothelial cell proliferation;
KW T-lymphocyte proliferation; endothelial cell apoptosis;
KW c-fos stimulation; pancreatic beta cell differentiation;
KW chondrocyte proliferation; glucose uptake; free fatty acid; FFA uptake;
KW tissue typing.
XX
OS Homo sapiens.
XX
PN US2003044844-A1.
XX
PD 06-MAR-2003.
XX
PF 01-FEB-2002; 2002US-00066211.
XX
PR 26-AUG-1997; 97US-0056974P.
PR 17-SEP-1997; 97US-0059115P.
PR 18-SEP-1997; 97US-0059263P.
PR 19-SEP-1997; 97US-0059588P.
PR 17-OCT-1997; 97US-0062885P.
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PR 27-OCT-1997; 97US-0063329P.
PR 29-OCT-1997; 97US-0063733P.
PR 21-NOV-1997; 97US-0066364P.
PR 25-NOV-1997; 97US-0066840P.
PR 16-DEC-1997; 97US-0069694P.
PR 09-FEB-1998; 98US-0074086P.
PR 09-FEB-1998; 98US-0074092P.
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PR 14-JUL-1998; 98WO-US014552.
PR 10-AUG-1998; 98US-0095998P.
PR 18-AUG-1998; 98US-0097000P.
PR 09-SEP-1998; 98US-0099601P.
PR 10-SEP-1998; 98US-0099803P.
PR 10-SEP-1998; 98US-0099811P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 16-SEP-1998; 98WO-US019330.
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PR 17-SEP-1998; 98WO-US019437.
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PR 20-NOV-1998; 98US-0109304P.
PR 20-NOV-1998; 98WO-US024855.
PR 25-NOV-1998; 98WO-US025190.
PR 01-DEC-1998; 98WO-US025108.
PR 08-MAR-1999; 99WO-US005028.
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PR 02-JUN-1999; 99WO-US012252.
PR 15-JUN-1999; 99US-0139695P.
PR 20-JUL-1999; 99US-0145070P.
PR 26-JUL-1999; 99US-0145698P.
PR 17-AUG-1999; 99US-0149396P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028565.
PR 07-DEC-1999; 99US-0169495P.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 09-MAR-2000; 2000WO-US006471.
PR 20-MAR-2000; 2000WO-US007377.
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PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 30-MAY-2001; 2001WO-US017443.
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PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 15-NOV-2001; 2001US-00002796.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;

PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
PI Wood WI, Zhang Z;
XX
DR WPI; 2003-615775/58.
DR N-PSDB; ADA47180.
XX
PT Novel isolated PRO polypeptides e.g. PRO365 and PRO187, useful for
PT inducing redifferentiation and/or proliferation of chondrocytes, and for
PT modulating glucose or free fatty acid uptake by skeletal muscle cells.
XX
PS Claim 12; Fig 3; 254pp; English.
XX
CC The invention relates to an isolated secreted/transmembrane PRO
CC polypeptide. The polypeptide and its nucleic acid is useful as an
CC inhibitor of vascular endothelial growth factor stimulated proliferation
CC of endothelial cells, as a stimulator of T-lymphocyte proliferation, as
CC an inducer of endothelial cell apoptosis, c-fos and differentiation of
CC pancreatic beta cell precursors into mature cell, for induction of
CC redifferentiation and/or proliferation of chondrocytes and for modulating
CC glucose or free fatty acid (FFA) uptake by skeletal muscle cells. The
CC polypeptide and its nucleic acid is useful for generating transgenic or
CC knock-out animals, for tissue typing and for chromosome identification.
CC The polypeptide is useful in a number of functional biological assays, as
CC molecular weight marker for protein electrophoresis, and as therapeutic
CC agents. The nucleic acid is useful as a hybridisation probe, in
CC chromosome and gene mapping, in the generation of antisense RNA and DNA,
CC and for the preparation PRO polypeptides. The nucleic acid is also useful
CC as hybridisation probe for a cDNA library to isolate the full length PRO
CC cDNA, to isolate other cDNA and in gene therapy. The nucleic acid is also
CC useful in the construction of hybridisation probes for mapping the gene
CC encoding PRO, and for the genetic analysis of individuals with the
CC genetic disorders. The present sequence represents the amino acid
CC sequence of a human secreted/transmembrane PRO polypeptide.
XX
SQ Sequence 117 AA;

Query Match 100.0%; Score 609; DB 6; Length 117;
Best Local Similarity 100.0%; Pred. No. 2e-63;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDK 117
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RESULT 9
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ID ABO44436 standard; protein; 117 AA.
XX
AC ABO44436;
XX
DT 01-OCT-2003 (first entry)
XX
DE Human secreted/transmembrane protein PRO444.
XX
KW Human; secreted protein; transmembrane protein; PRO; vulnerary; cardiant;
KW antidiabetic; anorectic; antiarthritic; angiogenesis; cancer;
KW adrenal cortical capillary; endothelial cell growth; wound healing;
KW stimulated T-lymphocyte proliferation; immune response suppression;
KW neonatal heart hypertrophy; cardiac insufficiency disorder;
KW vascular endothelial growth factor; inflammation; mononuclear cell;
KW eosinophil; diabetes; obesity; or hyper-insulinaemia; hypo-insulinaemia;
KW chondrocyte redifferentiation; bone disorder; cartilage disorder;
KW sports injury; arthritis.
XX
OS Homo sapiens.
XX

PN US2003044841-A1.
XX
PD 06-MAR-2003.
XX
PF 06-DEC-2001; 2001US-00006856.
XX
PR 01-SEP-1998; 98US-0098716P.
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PR 02-SEP-1998; 98US-0098843P.
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PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103449P.
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PR 07-OCT-1998; 98US-0103328P.
PR 07-OCT-1998; 98US-0103395P.
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PR 08-OCT-1998; 98US-0103633P.
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PR 14-OCT-1998; 98US-0104257P.
PR 20-OCT-1998; 98US-0104987P.
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PR 20-OCT-1998; 98US-0105002P.
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PR 10-NOV-1998; 98US-0107783P.
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PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.
PR 22-DEC-1998; 98US-0113296P.
PR 30-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 99WO-US000106.
PR 16-APR-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021194.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX
DR WPI; 2003-492259/46.
DR N-PSDB; ACH04344.
XX
PT Novel secreted and transmembrane polypeptides and polynucleotides
PT encoding them useful for treating various cardiac insufficiency
PT disorders, bone and/or cartilage disorders such as sports injuries and
PT arthritis.

Query Match 100.0%; Score 609; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 2e-63;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDK 117
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RESULT 10
ABO33460
ID ABO33460 standard; protein; 117 AA.
XX
AC ABO33460;
XX
DT 17-SEP-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO444.
XX
KW Human; secreted and transmembrane protein; PRO; gene therapy; vaccine;
KW tissue typing; chromosome identification; vaccine.
XX
OS Homo sapiens.
XX
PN US2003073129-A1.
XX
PD 17-APR-2003.
XX
PF 04-SEP-2001; 2001US-00946374.
XX
PR 01-SEP-1998; 98US-0098716P.
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PR 10-NOV-1998; 98US-0107783P.
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PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
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PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.

PR 24-AUG-2000; 2000WO-US023328.
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PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 14-JUN-2001; 2001US-00882636.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX
DR WPI; 2003-585292/55.
DR N-PSDB; ACD67888.
XX
PT Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful in the
PT preparation of a medicament for treating a condition responsive to PRO
PT polypeptide, and as therapeutic agents e.g. vaccines.
XX
PS Claim 12; Fig 4; 561pp; English.
XX
CC The invention describes an isolated PRO (secreted and transmembrane)
CC polypeptide (I), having at least 80% sequence identity to a sequence

Query Match 100.0%; Score 609; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 2e-63;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQ 60

Qy         61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDK 117
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Db         61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDK 117
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RESULT 11
ABO19838
ID ABO19838 standard; protein; 117 AA.
XX
AC ABO19838;
XX
DT 29-AUG-2003 (first entry)
XX
DE Human secreted/transmembrane protein PRO444.
XX
KW Human; PRO; secreted and transmembrane protein; gene therapy;
KW enterocolitis; gastrointestinal ulceration; skin disease; asthma;
KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
KW squamous cell carcinoma; Alzheimer's disease; Parkinson's disease;
KW amyotrophic lateral sclerosis; inflammatory disease; organ failure;
KW rheumatoid arthritis; multiple sclerosis; atherosclerosis; infertility;
KW cardiac injury; birth defect; premature aging; AIDS; cancer;
KW diabetic complication; wound repair.
XX
OS Homo sapiens.
XX
PN US2003044902-A1.
XX
PD 06-MAR-2003.
XX
PF 01-FEB-2002; 2002US-00066193.
XX
PR 26-AUG-1997; 97US-0056974P.
PR 17-SEP-1997; 97US-0059115P.
PR 18-SEP-1997; 97US-0059263P.
PR 19-SEP-1997; 97US-0059588P.
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PR 24-OCT-1997; 97US-0063082P.
PR 27-OCT-1997; 97US-0063329P.
PR 29-OCT-1997; 97US-0063733P.
PR 21-NOV-1997; 97US-0066364P.
PR 25-NOV-1997; 97US-0066840P.
PR 16-DEC-1997; 97US-0069694P.
PR 09-FEB-1998; 98US-0074086P.
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PR 09-SEP-1998; 98US-0099601P.
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PR 28-OCT-1998; 98US-0106032P.
PR 20-NOV-1998; 98US-0109304P.
PR 20-NOV-1998; 98WO-US024855.
PR 25-NOV-1998; 98WO-US025190.
PR 01-DEC-1998; 98WO-US025108.
PR 08-MAR-1999; 99WO-US005028.
PR 23-MAR-1999; 99US-0125778P.
PR 02-JUN-1999; 99WO-US012252.
PR 15-JUN-1999; 99US-0139695P.
PR 20-JUL-1999; 99US-0145070P.
PR 26-JUL-1999; 99US-0145698P.
PR 17-AUG-1999; 99US-0149396P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028565.
PR 07-DEC-1999; 99US-0169495P.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 09-MAR-2000; 2000WO-US006471.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 15-NOV-2001; 2001US-00002796.
XX

PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
PI Wood WI, Zhang Z;
XX
DR WPI; 2003-492261/46.
DR N-PSDB; ACD30202.
XX
PT New PRO polypeptides and nucleic acid molecules, useful in diagnosing or
PT treating inflammatory diseases, organ failure, atherosclerosis, cardiac
PT injury, infertility, cancer, AIDS, Alzheimer's disease or Parkinson's
PT disease.
XX
PS Claim 21; Fig 4; 154pp; English.
XX
CC The invention relates to an isolated native sequence PRO polypeptide
CC (secreted and transmembrane protein) having 80% sequence similarity to
CC one of 37 proteins sequences (or PRO lacking its signal peptide, a PRO
CC extracellular domain (with or without a signal peptide) encoded by a
CC nucleic acids 80% identical to one of 37 cDNA sequences, shown in the
CC specification. Also included are vectors comprising the PRO nucleic
CC acids, host cells comprising the vectors (used to produce the PRO
CC proteins), a chimaeric molecule comprising the PRO polypeptide fused to a
CC heterologous amino acid sequence, an anti-PRO antibody, linking a
CC bioactive molecule to a cell expressing the PRO polypeptides and
CC modulating at least one biological activity of a cell expressing the
CC polypeptides. The PRO polypeptides and nucleic acids are useful in
CC diagnosing or treating enterocolitis, gastrointestinal ulceration, skin
CC diseases associated with abnormal keratinocyte differentiation, e.g.
CC psoriasis or epithelial cancers such as squamous cell carcinoma,
CC Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis,
CC inflammatory diseases, e.g. rheumatoid arthritis, asthma or multiple
CC sclerosis, organ failure, atherosclerosis, cardiac injury, infertility,
CC birth defects, premature aging, AIDS, cancer, diabetic complications, or
CC mutations in general. The polypeptides are also useful for wound repair
CC and associated therapies concerned with re-growth of tissue. The
CC nucleotide sequences may be used as hybridisation probes in chromosome
CC and gene mapping, or in generating antisense RNA and DNA. PRO nucleic
CC acids are also useful in preparing PRO polypeptides, in assays to
CC identify other proteins or molecules involved in binding reaction, to
CC generate transgenic animals or knockout animals, which in turn are useful
CC in the development and screening of therapeutically useful reagents, for
CC chromosome identification, and tissue typing. The PRO polypeptides and
CC nucleic acid molecules are also useful in gene therapy, and as molecular
CC weight markers for protein electrophoresis purposes. The anti-PRO
CC antibodies may be used in diagnostic assays for PRO, or for the affinity
CC purification of PRO from recombinant cell culture or natural sources. The
CC present sequence represents a PRO protein of the invention
XX
SQ Sequence 117 AA;

Query Match 100.0%; Score 609; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 2e-63;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 12
ADC17875
ID ADC17875 standard; protein; 117 AA.
XX
AC ADC17875;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human PRO polypeptide #2.
XX
KW Human; PRO; protein electrophoresis; chromosome mapping; gene mapping;
KW genetic disorder.
XX
OS Homo sapiens.
XX
PN US2003064925-A1.
XX
PD 03-APR-2003.
XX
PF 10-DEC-2001; 2001US-00013907.
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PR 02-MAR-2000; 2000WO-US005841.
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PR 02-JUN-2000; 2000WO-US015264.
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PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX
DR WPI; 2003-555602/52.
DR N-PSDB; ADC17874.
XX
PT Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful in the
PT preparation of a medicament for treating a condition responsive to PRO
PT polypeptide, and as therapeutic agents e.g. vaccines.
XX
PS Claim 12; SEQ ID NO 6; 555pp; English.
XX
CC The invention relates to human PRO polypeptides and the polynucleotides
CC encoding them. The sequences are useful in the preparation of a
CC medicament for treating a condition responsive to a PRO polypeptide. The
CC polypeptides are useful in a number of functional biological assays, as
CC molecular weight markers for protein electrophoresis and as therapeutic

Query Match 100.0%; Score 609; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 2e-63;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQ 60
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Db          1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQ 60

Qy         61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDK 117
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDK 117
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RESULT 13
ADD10295
ID ADD10295 standard; protein; 117 AA.
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AC ADD10295;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human secreted/transmembrane PRO polypeptide #3.

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XX
KW   human; secreted protein; transmembrane protein; cardiovascular disorder;
KW   endothelial disorder; angiogenic disorder; myocardial infarction;
KW   cardiac hypertrophy; trauma; cancer; age-related macular degeneration;
KW   angiogenesis; endothelial cell apoptosis; smooth muscle cell growth;
KW   endothelial cell tube formation.
XX
OS   Homo sapiens.
XX
PN   US2003105011-A1.
XX
PD   05-JUN-2003.
XX
PF   16-AUG-2002; 2002US-00223084.
XX
PR   15-SEP-2000; 2000US-0232887P.
PR   20-JUN-2001; 2001WO-US019692.
PR   09-JUL-2001; 2001WO-US021735.
PR   20-FEB-2002; 2002US-00081056.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI   Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;
PI   Watanabe CK, Williams PM, Wood WI, Ye W;
XX
DR   WPI; 2003-810831/76.
DR   N-PSDB; ADD10294.
XX
PT   New isolated nucleic acid encoding a secreted and transmembrane
PT   polypeptide for treating a cardiovascular, endothelial, or angiogenic
PT   disorder in a mammal, such as cancer or age-related macular degeneration.
XX
PS   Claim 11; SEQ ID NO 6; 493pp; English.
XX
CC   The invention relates to an isolated nucleic acid encoding a secreted and
CC   transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded
CC   by the nucleic acid, or an agonist or antagonist, is used to treat a
CC   cardiovascular, endothelial, or angiogenic disorder in a mammal,
CC   preferably a human. The human may have suffered a myocardial infarction
CC   or has cardiac hypertrophy, trauma, a cancer, or age-related macular
CC   degeneration. The cardiac hypertrophy is characterised by the presence of
CC   an elevated level of PGF-2 alpha. A PRO polypeptide, given in the
CC   specification, or an agonist is used to inhibit or stimulate endothelial
CC   cell growth in a mammal. PRO21 or an agonist is used to induce cardiac
CC   hypertrophy. PRO1376 or PRO1449 is used to stimulate angiogenesis.
CC   PRO4302 or an agonist is used to induce endothelial cell apoptosis. A PRO
CC   polypeptide, given in the specification, or an agonist is used to
CC   stimulate or inhibit smooth muscle cell growth, or to induce endothelial
CC   cell tube formation. The present sequence represents the amino acid
CC   sequence of a PRO polypeptide of the invention.
XX
SQ   Sequence 117 AA;

  Query Match             100.0%;  Score 609;  DB 7;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 2e-63;
  Matches  117;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQ 60
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Db          1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQ 60

Qy         61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDK 117
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Db         61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDK 117


RESULT 14
ADD11255
ID   ADD11255 standard; protein; 117 AA.
XX
AC   ADD11255;
XX
DT   01-JAN-2004  (first entry)
XX
DE   Human secreted/transmembrane PRO polypeptide #3.
XX
KW   human; secreted protein; transmembrane protein; cardiovascular disorder;
KW   endothelial disorder; angiogenic disorder; myocardial infarction;
KW   cardiac hypertrophy; trauma; cancer; age-related macular degeneration;
KW   angiogenesis; endothelial cell apoptosis; smooth muscle cell growth;
KW   endothelial cell tube formation.
XX
OS   Homo sapiens.
XX
PN   US2003105013-A1.
XX
PD   05-JUN-2003.
XX
PF   16-AUG-2002; 2002US-00223090.
XX
PR   20-JUN-2001; 2001WO-US019692.
PR   09-JUL-2001; 2001WO-US021735.
PR   20-FEB-2002; 2002US-00081056.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI   Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;
PI   Watanabe CK, Williams PM, Wood WI, Ye W;
XX
DR   WPI; 2003-801242/75.
DR   N-PSDB; ADD11254.
XX
PT   New isolated nucleic acid encoding a secreted and transmembrane
PT   polypeptide, useful for treating a cardiovascular, endothelial, or
PT   angiogenic disorder in a mammal, such as cancer or age-related macular
PT   degeneration.
XX
PS   Claim 11; SEQ ID NO 6; 493pp; English.
XX
CC   The invention relates to an isolated nucleic acid encoding a secreted and
CC   transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded
CC   by the nucleic acid, or an agonist or antagonist, is used to treat a
CC   cardiovascular, endothelial, or angiogenic disorder in a mammal,
CC   preferably a human. The human may have suffered a myocardial infarction
CC   or has cardiac hypertrophy, trauma, a cancer, or age-related macular
CC   degeneration. The cardiac hypertrophy is characterised by the presence of
CC   an elevated level of PGF-2 alpha. A PRO polypeptide, given in the
CC   specification, or an agonist is used to inhibit or stimulate endothelial
CC   cell growth in a mammal. PRO21 or an agonist is used to induce cardiac
CC   hypertrophy. PRO1376 or PRO1449 is used to stimulate angiogenesis.
CC   PRO4302 or an agonist is used to induce endothelial cell apoptosis. A PRO
CC   polypeptide, given in the specification, or an agonist is used to
CC   stimulate or inhibit smooth muscle cell growth, or to induce endothelial
CC   cell tube formation. The present sequence represents the amino acid
CC   sequence of a PRO polypeptide of the invention.
XX
SQ   Sequence 117 AA;

  Query Match             100.0%;  Score 609;  DB 7;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 2e-63;
  Matches  117;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQ 60

Qy         61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDK 117
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 QQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDK 117


RESULT 15
ADD70521
ID   ADD70521 standard; protein; 117 AA.
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XX
AC ADD70521;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human secreted/transmembrane protein PRO444.
XX
KW Human; secreted protein; transmembrane protein; PRO; tumour;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW dermatitis; herpetiformis; Crohn's disease; thalassaemia.
XX
OS Homo sapiens.
XX
PN US2003099625-A1.
XX
PD 29-MAY-2003.
XX
PF 12-DEC-2001; 2001US-00015386.
XX
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 01-SEP-1998; 98US-0098749P.
PR 01-SEP-1998; 98US-0098750P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099536P.
PR 09-SEP-1998; 98US-0099596P.
PR 09-SEP-1998; 98US-0099598P.
PR 09-SEP-1998; 98US-0099602P.
PR 09-SEP-1998; 98US-0099642P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
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PR 16-SEP-1998; 98US-0100584P.
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PR 22-SEP-1998; 98US-0101279P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101474P.
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PR 18-NOV-1998; 98US-0108851P.
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PR 05-JAN-1999; 99WO-US000106.
PR 16-APR-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021194.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX
DR WPI; 2003-874602/81.
DR N-PSDB; ADD70520.
XX
PT Novel isolated PRO polypeptides e.g., PRO1130, PRO1275, PRO1418, PRO1555,
PT PRO1787 affect glucose or free fatty acid (FFA) uptake by skeletal muscle
PT cells and are useful for treating diabetes or hyper- or hypo-insulinemia.
XX
PS Claim 12; SEQ ID NO 6; 553pp; English.
XX
CC The invention relates to an isolated PRO polypeptide (secreted or

Query Match 100.0%; Score 609; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 2e-63;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Job time : 57 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 4, 2004; 06:40:17 ; Search time 504 Seconds
(without alignments)
9038.793 Million cell updates/sec

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Perfect score: 1218
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2466186 seqs, 1870095128 residues

Total number of hits satisfying chosen parameters: 4932372

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1218	100.0	1218	10	US-09-946-374-5	Sequence 5, Appli
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4	1218	100.0	1218	14	US-10-002-796-8	Sequence 8, Appli
5	1218	100.0	1218	14	US-10-066-273-8	Sequence 8, Appli
6	1218	100.0	1218	14	US-10-066-494-8	Sequence 8, Appli
7	1218	100.0	1218	14	US-10-066-269-8	Sequence 8, Appli
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ALIGNMENTS

RESULT 1
US-09-946-374-5
; Sequence 5, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C1
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Qy       1201 CTATGATCTTTATTAGAG 1218
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Db       1201 CTATGATCTTTATTAGAG 1218


RESULT 2
US-10-081-056-5
; Sequence 5, Application US/10081056
; Publication No. US20040043927A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Marsters, Scot A.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Stephan, Jean-Philippe F.
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Williams, P.Mickey
;  APPLICANT:  Ye, Weilan
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
;  TITLE OF INVENTION:  TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
;  FILE REFERENCE: P3235P1C1
;  CURRENT APPLICATION NUMBER: US/10/081,056
;  CURRENT FILING DATE:  2002-02-20
;  PRIOR APPLICATION NUMBER: PCT/US01/21735
;  PRIOR FILING DATE: 2001-07-09
;  PRIOR APPLICATION NUMBER: US 60/219,556
;  PRIOR FILING DATE: 2000-07-20
;  PRIOR APPLICATION NUMBER: US 60/220,624
;  PRIOR FILING DATE: 2000-07-25
;  PRIOR APPLICATION NUMBER: US 60/220,664
;  PRIOR FILING DATE: 2000-07-25
;  PRIOR APPLICATION NUMBER: PCT/US00/20710
;  PRIOR FILING DATE: 2000-07-28
;  PRIOR APPLICATION NUMBER: US 60/222,695
;  PRIOR FILING DATE: 2000-08-02
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; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
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; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/230,978
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/000,000
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 09/664,610
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/242,922
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 09/709,238
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: PCT/US00/30952
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: PCT/US00/30873
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; PRIOR FILING DATE: 2000-12-01
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; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: US 09/796,498
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; PRIOR APPLICATION NUMBER: PCT/US01/06666
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; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 09/828,366
; PRIOR FILING DATE: 2001-04-05
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; PRIOR APPLICATION NUMBER: US 09/870,574
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; PRIOR APPLICATION NUMBER: PCT/US01/17443
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/00000
; PRIOR FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 5
; LENGTH: 1218
; TYPE: DNA
; ORGANISM: Homosapiens
US-10-081-056-5

Query Match 100.0%; Score 1218; DB 12; Length 1218;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACA 60
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Db          1 CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACA 60

Qy         61 AAGGAGTCGCGCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGT 120
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Db         61 AAGGAGTCGCGCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGT 120

Qy        121 CAGTGCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCT 180
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Db        121 CAGTGCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCT 180

Qy        181 GAGGGTTGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACC 240
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Db        181 GAGGGTTGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACC 240

Qy        241 GGACTGGGGCCGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAAC 300
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Qy        301 CTGAGAAACAGCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTC 360
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Db        301 CTGAGAAACAGCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTC 360

Qy        361 CTAGAAGAGGGTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCC 420
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Db        361 CTAGAAGAGGGTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCC 420

Qy        421 CTTCTGAGGAGGCTGCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCT 480
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Db        421 CTTCTGAGGAGGCTGCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCT 480

Qy        481 GTAGTTGATAATGTTGGGAATAAGCTCTGCAACTTTCTTTGGCATTCAGTTGTTAAAAAC 540
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Db        481 GTAGTTGATAATGTTGGGAATAAGCTCTGCAACTTTCTTTGGCATTCAGTTGTTAAAAAC 540

Qy        541 AAATAGGATGCAAATTCCTCAACTCCAGGTTATGAAAACAGTACTTGGAAAACTGAAAAC 600
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Db        541 AAATAGGATGCAAATTCCTCAACTCCAGGTTATGAAAACAGTACTTGGAAAACTGAAAAC 600

Qy        601 TACCTAAATGATCGTCTTTGGTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGG 660
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Db        601 TACCTAAATGATCGTCTTTGGTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGG 660

Qy        661 TCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTAC 720
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Db        661 TCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTAC 720

Qy        721 TACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACAC 780
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Db        721 TACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACAC 780

Qy        781 CCAACAGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACACAAGGAGCCAACCACG 840
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Db        781 CCAACAGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACACAAGGAGCCAACCACG 840

Qy        841 GGACCCTGTTCGGCCACCAAGGAGGGGCCGAGGACCTCATGAGCCAAGGAGAAAGAAACA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGACCCTGTTCGGCCACCAAGGAGGGGCCGAGGACCTCATGAGCCAAGGAGAAAGAAACA 900

Qy        901 AAATGTGGATGGGCTAGTGTTGGACACACTGGCAGTAATACGGACTCTTGTAGATAAGTA 960
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Db        901 AAATGTGGATGGGCTAGTGTTGGACACACTGGCAGTAATACGGACTCTTGTAGATAAGTA 960

Qy        961 AGTATCTGACTCACGGTCACCTCCAGTGGAATGAAAAGTGTTCTGCCCGGAACCATGACT 1020
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Db        961 AGTATCTGACTCACGGTCACCTCCAGTGGAATGAAAAGTGTTCTGCCCGGAACCATGACT 1020

Qy       1021 TTAGGACTCCTTCAGTTCCTTTAGGACATACTCGCCAAGCCTTGTGCTCACAGGGCAAAG 1080
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Db       1081 GAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAATGATAAGATTTGATGTTTTTGCTT 1140

Qy       1141 GCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTCTGTAGCAGAAAACACGATAAAG 1200
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Db       1141 GCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTCTGTAGCAGAAAACACGATAAAG 1200

Qy       1201 CTATGATCTTTATTAGAG 1218
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Db       1201 CTATGATCTTTATTAGAG 1218
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RESULT 3
US-10-066-500-8
; Sequence 8, Application US/10066500
; Publication No. US20020177165A1
; GENERAL INFORMATION:
; APPLICANT: Avi J. Ashkenazi
; APPLICANT: Kevin P. Baker
; APPLICANT: David A. Botstein
; APPLICANT: Luc Desnoyers
; APPLICANT: Dan L. Eaton
; APPLICANT: Napoleone Ferrara
; APPLICANT: Sherman Fong
; APPLICANT: Wei-Qiang Gao
; APPLICANT: Hanspeter Gerber
; APPLICANT: Mary E. Gerritsen
; APPLICANT: Audrey Goddard
; APPLICANT: Paul J. Godowski
; APPLICANT: Austin L. Gurney
; APPLICANT: Ivar J. Kljavin
; APPLICANT: Jennie P. Mather
; APPLICANT: Mary A. Napier
; APPLICANT: James Pan
; APPLICANT: Nicholas F. Paoni
; APPLICANT: Margaret Ann Roy
; APPLICANT: Timothy A. Stewart
; APPLICANT: Daniel Tumas
; APPLICANT: Colin K. Watanabe
; APPLICANT: P.Mickey Williams
; APPLICANT: William I. Wood
; APPLICANT: Zemin Zang
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3130R1C7
; CURRENT APPLICATION NUMBER: US/10/066,500
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 10/002,796
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
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; PRIOR APPLICATION NUMBER: 60/062285
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/062816
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; PRIOR APPLICATION NUMBER: 60/063082
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; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: PCT/US99/20111
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547

Query Match 100.0%; Score 1218; DB 13; Length 1218;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      61 AAGGAGTCGCGCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGT 120
Db      61 AAGGAGTCGCGCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGT 120

Qy     121 CAGTGCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCT 180
Db     121 CAGTGCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCT 180

Qy     181 GAGGGTTGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACC 240
Db     181 GAGGGTTGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACC 240

Qy     241 GGACTGGGGCCGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAAC 300
Db     241 GGACTGGGGCCGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAAC 300

Qy     301 CTGAGAAACAGCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTC 360
Db     301 CTGAGAAACAGCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTC 360

Qy     361 CTAGAAGAGGGTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCC 420
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Db     421 CTTCTGAGGAGGCTGCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCT 480

Qy     481 GTAGTTGATAATGTTGGGAATAAGCTCTGCAACTTTCTTTGGCATTCAGTTGTTAAAAAC 540
Db     481 GTAGTTGATAATGTTGGGAATAAGCTCTGCAACTTTCTTTGGCATTCAGTTGTTAAAAAC 540

Qy     541 AAATAGGATGCAAATTCCTCAACTCCAGGTTATGAAAACAGTACTTGGAAAACTGAAAAC 600
Db     541 AAATAGGATGCAAATTCCTCAACTCCAGGTTATGAAAACAGTACTTGGAAAACTGAAAAC 600

Qy     601 TACCTAAATGATCGTCTTTGGTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGG 660
Db     601 TACCTAAATGATCGTCTTTGGTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGG 660

Qy     661 TCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTAC 720
Db     661 TCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTAC 720

Qy     721 TACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACAC 780
Db     721 TACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACAC 780

Qy     781 CCAACAGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACACAAGGAGCCAACCACG 840
Db     781 CCAACAGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACACAAGGAGCCAACCACG 840

Qy     841 GGACCCTGTTCGGCCACCAAGGAGGGGCCGAGGACCTCATGAGCCAAGGAGAAAGAAACA 900
Db     841 GGACCCTGTTCGGCCACCAAGGAGGGGCCGAGGACCTCATGAGCCAAGGAGAAAGAAACA 900

Qy     901 AAATGTGGATGGGCTAGTGTTGGACACACTGGCAGTAATACGGACTCTTGTAGATAAGTA 960
Db     901 AAATGTGGATGGGCTAGTGTTGGACACACTGGCAGTAATACGGACTCTTGTAGATAAGTA 960

Qy     961 AGTATCTGACTCACGGTCACCTCCAGTGGAATGAAAAGTGTTCTGCCCGGAACCATGACT 1020
Db     961 AGTATCTGACTCACGGTCACCTCCAGTGGAATGAAAAGTGTTCTGCCCGGAACCATGACT 1020

Qy    1021 TTAGGACTCCTTCAGTTCCTTTAGGACATACTCGCCAAGCCTTGTGCTCACAGGGCAAAG 1080
Db    1021 TTAGGACTCCTTCAGTTCCTTTAGGACATACTCGCCAAGCCTTGTGCTCACAGGGCAAAG 1080
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RESULT 4
US-10-002-796-8
; Sequence 8, Application US/10002796
; Publication No. US20030032057A1
; GENERAL INFORMATION:
; APPLICANT: Avi J. Ashkenazi
; APPLICANT: Kevin P. Baker
; APPLICANT: David A. Botstein
; APPLICANT: Luc Desnoyers
; APPLICANT: Dan L. Eaton
; APPLICANT: Napoleone Ferrara
; APPLICANT: Sherman Fong
; APPLICANT: Wei-Qiang Gao
; APPLICANT: Hanspeter Gerber
; APPLICANT: Mary E. Gerritsen
; APPLICANT: Audrey Goddard
; APPLICANT: Paul J. Godowski
; APPLICANT: Austin L. Gurney
; APPLICANT: Ivar J. Kljavin
; APPLICANT: Jennie P. Mather
; APPLICANT: Mary A. Napier
; APPLICANT: James Pan
; APPLICANT: Nicholas F. Paoni
; APPLICANT: Margaret Ann Roy
; APPLICANT: Timothy A. Stewart
; APPLICANT: Daniel Tumas
; APPLICANT: Colin K. Watanabe
; APPLICANT: P.Mickey Williams
; APPLICANT: William I. Wood
; APPLICANT: Zemin Zang
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3130R1C1
; CURRENT APPLICATION NUMBER: US/10/002,796
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
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; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/28301

Query Match 100.0%; Score 1218; DB 14; Length 1218;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db         61 AAGGAGTCGCGCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGT 120

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Db        181 GAGGGTTGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACC 240

Qy        241 GGACTGGGGCCGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAAC 300
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Db        361 CTAGAAGAGGGTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCC 420

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Db        661 TCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTAC 720

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RESULT 5
US-10-066-273-8
; Sequence 8, Application US/10066273
; Publication No. US20030032062A1
; GENERAL INFORMATION:
; APPLICANT: Avi J. Ashkenazi
; APPLICANT: Kevin P. Baker
; APPLICANT: David A. Botstein
; APPLICANT: Luc Desnoyers
; APPLICANT: Dan L. Eaton
; APPLICANT: Napoleone Ferrara
; APPLICANT: Sherman Fong
; APPLICANT: Wei-Qiang Gao
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; APPLICANT: Mary E. Gerritsen
; APPLICANT: Audrey Goddard
; APPLICANT: Paul J. Godowski
; APPLICANT: Austin L. Gurney
; APPLICANT: Ivar J. Kljavin
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; APPLICANT: Mary A. Napier
; APPLICANT: James Pan
; APPLICANT: Nicholas F. Paoni
; APPLICANT: Margaret Ann Roy
; APPLICANT: Timothy A. Stewart
; APPLICANT: Daniel Tumas
; APPLICANT: Colin K. Watanabe
; APPLICANT: P.Mickey Williams
; APPLICANT: William I. Wood
; APPLICANT: Zemin Zang
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3130R1C2
; CURRENT APPLICATION NUMBER: US/10/066,273
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 10/002,796
; PRIOR FILING DATE: 2001-11-15
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; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547

Query Match 100.0%; Score 1218; DB 14; Length 1218;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       1 CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACA 60

Qy      61 AAGGAGTCGCGCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGT 120
Db      61 AAGGAGTCGCGCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGT 120

Qy     121 CAGTGCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCT 180
Db     121 CAGTGCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCT 180

Qy     181 GAGGGTTGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACC 240
Db     181 GAGGGTTGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACC 240

Qy     241 GGACTGGGGCCGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAAC 300
Db     241 GGACTGGGGCCGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAAC 300

Qy     301 CTGAGAAACAGCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTC 360
Db     301 CTGAGAAACAGCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTC 360

Qy     361 CTAGAAGAGGGTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCC 420
Db     361 CTAGAAGAGGGTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCC 420

Qy     421 CTTCTGAGGAGGCTGCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCT 480
Db     421 CTTCTGAGGAGGCTGCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCT 480

Qy     481 GTAGTTGATAATGTTGGGAATAAGCTCTGCAACTTTCTTTGGCATTCAGTTGTTAAAAAC 540
Db     481 GTAGTTGATAATGTTGGGAATAAGCTCTGCAACTTTCTTTGGCATTCAGTTGTTAAAAAC 540

Qy     541 AAATAGGATGCAAATTCCTCAACTCCAGGTTATGAAAACAGTACTTGGAAAACTGAAAAC 600
Db     541 AAATAGGATGCAAATTCCTCAACTCCAGGTTATGAAAACAGTACTTGGAAAACTGAAAAC 600

Qy     601 TACCTAAATGATCGTCTTTGGTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGG 660
Db     601 TACCTAAATGATCGTCTTTGGTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGG 660

Qy     661 TCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTAC 720
Db     661 TCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTAC 720

Qy     721 TACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACAC 780
Db     721 TACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACAC 780

Qy     781 CCAACAGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACACAAGGAGCCAACCACG 840
Db     781 CCAACAGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACACAAGGAGCCAACCACG 840

Qy     841 GGACCCTGTTCGGCCACCAAGGAGGGGCCGAGGACCTCATGAGCCAAGGAGAAAGAAACA 900
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Qy     901 AAATGTGGATGGGCTAGTGTTGGACACACTGGCAGTAATACGGACTCTTGTAGATAAGTA 960
Db     901 AAATGTGGATGGGCTAGTGTTGGACACACTGGCAGTAATACGGACTCTTGTAGATAAGTA 960

Qy     961 AGTATCTGACTCACGGTCACCTCCAGTGGAATGAAAAGTGTTCTGCCCGGAACCATGACT 1020
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Qy    1021 TTAGGACTCCTTCAGTTCCTTTAGGACATACTCGCCAAGCCTTGTGCTCACAGGGCAAAG 1080
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Qy       1081 GAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAATGATAAGATTTGATGTTTTTGCTT 1140
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Qy       1201 CTATGATCTTTATTAGAG 1218
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RESULT 6
US-10-066-494-8
; Sequence 8, Application US/10066494
; Publication No. US20030032063A1
; GENERAL INFORMATION:
; APPLICANT: Avi J. Ashkenazi
; APPLICANT: Kevin P. Baker
; APPLICANT: David A. Botstein
; APPLICANT: Luc Desnoyers
; APPLICANT: Dan L. Eaton
; APPLICANT: Napoleone Ferrara
; APPLICANT: Sherman Fong
; APPLICANT: Wei-Qiang Gao
; APPLICANT: Hanspeter Gerber
; APPLICANT: Mary E. Gerritsen
; APPLICANT: Audrey Goddard
; APPLICANT: Paul J. Godowski
; APPLICANT: Austin L. Gurney
; APPLICANT: Ivar J. Kljavin
; APPLICANT: Jennie P. Mather
; APPLICANT: Mary A. Napier
; APPLICANT: James Pan
; APPLICANT: Nicholas F. Paoni
; APPLICANT: Margaret Ann Roy
; APPLICANT: Timothy A. Stewart
; APPLICANT: Daniel Tumas
; APPLICANT: Colin K. Watanabe
; APPLICANT: P.Mickey Williams
; APPLICANT: William I. Wood
; APPLICANT: Zemin Zang
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3130R1C9
; CURRENT APPLICATION NUMBER: US/10/066,494
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 10/002,796
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
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; PRIOR APPLICATION NUMBER: PCT/US99/20111
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547

Query Match 100.0%; Score 1218; DB 14; Length 1218;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACA 60
Db       1 CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACA 60

Qy      61 AAGGAGTCGCGCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGT 120
Db      61 AAGGAGTCGCGCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGT 120

Qy     121 CAGTGCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCT 180
Db     121 CAGTGCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCT 180

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Db     181 GAGGGTTGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACC 240

Qy     241 GGACTGGGGCCGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAAC 300
Db     241 GGACTGGGGCCGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAAC 300

Qy     301 CTGAGAAACAGCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTC 360
Db     301 CTGAGAAACAGCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTC 360

Qy     361 CTAGAAGAGGGTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCC 420
Db     361 CTAGAAGAGGGTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCC 420

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Db     421 CTTCTGAGGAGGCTGCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCT 480

Qy     481 GTAGTTGATAATGTTGGGAATAAGCTCTGCAACTTTCTTTGGCATTCAGTTGTTAAAAAC 540
Db     481 GTAGTTGATAATGTTGGGAATAAGCTCTGCAACTTTCTTTGGCATTCAGTTGTTAAAAAC 540

Qy     541 AAATAGGATGCAAATTCCTCAACTCCAGGTTATGAAAACAGTACTTGGAAAACTGAAAAC 600
Db     541 AAATAGGATGCAAATTCCTCAACTCCAGGTTATGAAAACAGTACTTGGAAAACTGAAAAC 600

Qy     601 TACCTAAATGATCGTCTTTGGTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGG 660
Db     601 TACCTAAATGATCGTCTTTGGTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGG 660

Qy     661 TCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTAC 720
Db     661 TCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTAC 720

Qy     721 TACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACAC 780
Db     721 TACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACAC 780

Qy     781 CCAACAGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACACAAGGAGCCAACCACG 840
Db     781 CCAACAGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACACAAGGAGCCAACCACG 840

Qy     841 GGACCCTGTTCGGCCACCAAGGAGGGGCCGAGGACCTCATGAGCCAAGGAGAAAGAAACA 900
Db     841 GGACCCTGTTCGGCCACCAAGGAGGGGCCGAGGACCTCATGAGCCAAGGAGAAAGAAACA 900

Qy     901 AAATGTGGATGGGCTAGTGTTGGACACACTGGCAGTAATACGGACTCTTGTAGATAAGTA 960
Db     901 AAATGTGGATGGGCTAGTGTTGGACACACTGGCAGTAATACGGACTCTTGTAGATAAGTA 960

Qy     961 AGTATCTGACTCACGGTCACCTCCAGTGGAATGAAAAGTGTTCTGCCCGGAACCATGACT 1020
Db     961 AGTATCTGACTCACGGTCACCTCCAGTGGAATGAAAAGTGTTCTGCCCGGAACCATGACT 1020

Qy    1021 TTAGGACTCCTTCAGTTCCTTTAGGACATACTCGCCAAGCCTTGTGCTCACAGGGCAAAG 1080
Db    1021 TTAGGACTCCTTCAGTTCCTTTAGGACATACTCGCCAAGCCTTGTGCTCACAGGGCAAAG 1080
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Db       1081 GAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAATGATAAGATTTGATGTTTTTGCTT 1140

Qy       1141 GCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTCTGTAGCAGAAAACACGATAAAG 1200
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Db       1141 GCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTCTGTAGCAGAAAACACGATAAAG 1200

Qy       1201 CTATGATCTTTATTAGAG 1218
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Db       1201 CTATGATCTTTATTAGAG 1218
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RESULT 7
US-10-066-269-8
; Sequence 8, Application US/10066269
; Publication No. US20030040014A1
; GENERAL INFORMATION:
; APPLICANT: Avi J. Ashkenazi
; APPLICANT: Kevin P. Baker
; APPLICANT: David A. Botstein
; APPLICANT: Luc Desnoyers
; APPLICANT: Dan L. Eaton
; APPLICANT: Napoleone Ferrara
; APPLICANT: Sherman Fong
; APPLICANT: Wei-Qiang Gao
; APPLICANT: Hanspeter Gerber
; APPLICANT: Mary E. Gerritsen
; APPLICANT: Audrey Goddard
; APPLICANT: Paul J. Godowski
; APPLICANT: Austin L. Gurney
; APPLICANT: Ivar J. Kljavin
; APPLICANT: Jennie P. Mather
; APPLICANT: Mary A. Napier
; APPLICANT: James Pan
; APPLICANT: Nicholas F. Paoni
; APPLICANT: Margaret Ann Roy
; APPLICANT: Timothy A. Stewart
; APPLICANT: Daniel Tumas
; APPLICANT: Colin K. Watanabe
; APPLICANT: P.Mickey Williams
; APPLICANT: William I. Wood
; APPLICANT: Zemin Zang
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3130R1C4
; CURRENT APPLICATION NUMBER: US/10/066,269
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 10/002,796
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059115
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; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 09/664610
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: 09/665350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: 09/709238
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; PRIOR APPLICATION NUMBER: 09/767609
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; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/US98/19093
; PRIOR FILING DATE: 1998-09-14
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: 1998-09-16
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; PRIOR FILING DATE: 1998-12-01
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; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: PCT/US99/05028
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: PCT/US99/20111
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547

Query Match 100.0%; Score 1218; DB 14; Length 1218;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       1 CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACA 60

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Qy     181 GAGGGTTGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACC 240
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Qy     241 GGACTGGGGCCGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAAC 300
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Qy     481 GTAGTTGATAATGTTGGGAATAAGCTCTGCAACTTTCTTTGGCATTCAGTTGTTAAAAAC 540
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Qy     601 TACCTAAATGATCGTCTTTGGTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGG 660
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Qy     661 TCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTAC 720
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Qy     721 TACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACAC 780
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Db       1201 CTATGATCTTTATTAGAG 1218
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RESULT 8
US-10-006-856A-5
; Sequence 5, Application US/10006856A
; Publication No. US20030044841A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C14
; CURRENT APPLICATION NUMBER: US/10/006,856A
; CURRENT FILING DATE: 2002-05-10
; NUMBER OF SEQ ID NOS: 477
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 5
; LENGTH: 1218
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-006-856A-5

Query Match 100.0%; Score 1218; DB 14; Length 1218;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        841 GGACCCTGTTCGGCCACCAAGGAGGGGCCGAGGACCTCATGAGCCAAGGAGAAAGAAACA 900
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RESULT 9
US-10-066-211-8
; Sequence 8, Application US/10066211
; Publication No. US20030044844A1
; GENERAL INFORMATION:
; APPLICANT: Avi J. Ashkenazi
; APPLICANT: Kevin P. Baker
; APPLICANT: David A. Botstein
; APPLICANT: Luc Desnoyers
; APPLICANT: Dan L. Eaton
; APPLICANT: Napoleone Ferrara

; APPLICANT: Sherman Fong
; APPLICANT: Wei-Qiang Gao
; APPLICANT: Hanspeter Gerber
; APPLICANT: Mary E. Gerritsen
; APPLICANT: Audrey Goddard
; APPLICANT: Paul J. Godowski
; APPLICANT: Austin L. Gurney
; APPLICANT: Ivar J. Kljavin
; APPLICANT: Jennie P. Mather
; APPLICANT: Mary A. Napier
; APPLICANT: James Pan
; APPLICANT: Nicholas F. Paoni
; APPLICANT: Margaret Ann Roy
; APPLICANT: Timothy A. Stewart
; APPLICANT: Daniel Tumas
; APPLICANT: Colin K. Watanabe
; APPLICANT: P.Mickey Williams
; APPLICANT: William I. Wood
; APPLICANT: Zemin Zang
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3130R1C8
; CURRENT APPLICATION NUMBER: US/10/066,211
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 10/002,796
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
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; PRIOR APPLICATION NUMBER: PCT/US99/20111
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547

Query Match 100.0%; Score 1218; DB 14; Length 1218;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACA 60
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Qy         61 AAGGAGTCGCGCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGT 120
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Qy        181 GAGGGTTGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACC 240
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Qy        241 GGACTGGGGCCGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAAC 300
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Qy        361 CTAGAAGAGGGTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCC 420
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Db        361 CTAGAAGAGGGTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCC 420

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Qy        481 GTAGTTGATAATGTTGGGAATAAGCTCTGCAACTTTCTTTGGCATTCAGTTGTTAAAAAC 540
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Qy        541 AAATAGGATGCAAATTCCTCAACTCCAGGTTATGAAAACAGTACTTGGAAAACTGAAAAC 600
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Db        601 TACCTAAATGATCGTCTTTGGTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGG 660

Qy        661 TCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTAC 720
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Db        661 TCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTAC 720

Qy        721 TACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACAC 780
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Db        721 TACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACAC 780

Qy        781 CCAACAGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACACAAGGAGCCAACCACG 840
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Db        781 CCAACAGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACACAAGGAGCCAACCACG 840

Qy        841 GGACCCTGTTCGGCCACCAAGGAGGGGCCGAGGACCTCATGAGCCAAGGAGAAAGAAACA 900
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Qy        961 AGTATCTGACTCACGGTCACCTCCAGTGGAATGAAAAGTGTTCTGCCCGGAACCATGACT 1020
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Db        961 AGTATCTGACTCACGGTCACCTCCAGTGGAATGAAAAGTGTTCTGCCCGGAACCATGACT 1020

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RESULT 10
US-10-066-193-8
; Sequence 8, Application US/10066193
; Publication No. US20030044902A1
; GENERAL INFORMATION:
; APPLICANT: Avi J. Ashkenazi
; APPLICANT: Kevin P. Baker
; APPLICANT: David A. Botstein
; APPLICANT: Luc Desnoyers
; APPLICANT: Dan L. Eaton
; APPLICANT: Napoleone Ferrara

; APPLICANT: Sherman Fong
; APPLICANT: Wei-Qiang Gao
; APPLICANT: Hanspeter Gerber
; APPLICANT: Mary E. Gerritsen
; APPLICANT: Audrey Goddard
; APPLICANT: Paul J. Godowski
; APPLICANT: Austin L. Gurney
; APPLICANT: Ivar J. Kljavin
; APPLICANT: Jennie P. Mather
; APPLICANT: Mary A. Napier
; APPLICANT: James Pan
; APPLICANT: Nicholas F. Paoni
; APPLICANT: Margaret Ann Roy
; APPLICANT: Timothy A. Stewart
; APPLICANT: Daniel Tumas
; APPLICANT: Colin K. Watanabe
; APPLICANT: P.Mickey Williams
; APPLICANT: William I. Wood
; APPLICANT: Zemin Zang
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3130R1C3
; CURRENT APPLICATION NUMBER: US/10/066,193
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 10/002,796
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059115
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; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: PCT/US98/14552
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; PRIOR APPLICATION NUMBER: PCT/US98/18824
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/US98/19093
; PRIOR FILING DATE: 1998-09-14
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: 1998-09-16
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; PRIOR APPLICATION NUMBER: PCT/US99/05028
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: PCT/US99/20111
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547

Query Match 100.0%; Score 1218; DB 14; Length 1218;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACA 60
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Db          1 CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACA 60

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Qy        241 GGACTGGGGCCGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAAC 300
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Qy        361 CTAGAAGAGGGTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCC 420
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Db        361 CTAGAAGAGGGTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCC 420

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Qy        661 TCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTAC 720
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Db        661 TCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTAC 720

Qy        721 TACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACAC 780
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Db        721 TACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACAC 780

Qy        781 CCAACAGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACACAAGGAGCCAACCACG 840
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Db        781 CCAACAGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACACAAGGAGCCAACCACG 840

Qy        841 GGACCCTGTTCGGCCACCAAGGAGGGGCCGAGGACCTCATGAGCCAAGGAGAAAGAAACA 900
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Qy        901 AAATGTGGATGGGCTAGTGTTGGACACACTGGCAGTAATACGGACTCTTGTAGATAAGTA 960
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Db        901 AAATGTGGATGGGCTAGTGTTGGACACACTGGCAGTAATACGGACTCTTGTAGATAAGTA 960

Qy        961 AGTATCTGACTCACGGTCACCTCCAGTGGAATGAAAAGTGTTCTGCCCGGAACCATGACT 1020
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Db        961 AGTATCTGACTCACGGTCACCTCCAGTGGAATGAAAAGTGTTCTGCCCGGAACCATGACT 1020

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RESULT 11
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; Sequence 5, Application US/10006818A
; Publication No. US20030054406A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan 1.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman

```
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C4
;  CURRENT APPLICATION NUMBER: US/10/006,818A
;  CURRENT FILING DATE:  2001-12-06
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 5
;   LENGTH: 1218
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-006-818A-5

  Query Match            100.0%;  Score 1218;  DB 14;  Length 1218;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1218;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        421 CTTCTGAGGAGGCTGCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCT 480
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTAGTTGATAATGTTGGGAATAAGCTCTGCAACTTTCTTTGGCATTCAGTTGTTAAAAAC 540

Qy        541 AAATAGGATGCAAATTCCTCAACTCCAGGTTATGAAAACAGTACTTGGAAAACTGAAAAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AAATAGGATGCAAATTCCTCAACTCCAGGTTATGAAAACAGTACTTGGAAAACTGAAAAC 600

Qy        601 TACCTAAATGATCGTCTTTGGTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TACCTAAATGATCGTCTTTGGTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGG 660

Qy        661 TCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTAC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTAC 720

Qy        721 TACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACAC 780

Qy        781 CCAACAGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACACAAGGAGCCAACCACG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CCAACAGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACACAAGGAGCCAACCACG 840

Qy        841 GGACCCTGTTCGGCCACCAAGGAGGGGCCGAGGACCTCATGAGCCAAGGAGAAAGAAACA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGACCCTGTTCGGCCACCAAGGAGGGGCCGAGGACCTCATGAGCCAAGGAGAAAGAAACA 900

Qy        901 AAATGTGGATGGGCTAGTGTTGGACACACTGGCAGTAATACGGACTCTTGTAGATAAGTA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AAATGTGGATGGGCTAGTGTTGGACACACTGGCAGTAATACGGACTCTTGTAGATAAGTA 960

Qy        961 AGTATCTGACTCACGGTCACCTCCAGTGGAATGAAAAGTGTTCTGCCCGGAACCATGACT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGTATCTGACTCACGGTCACCTCCAGTGGAATGAAAAGTGTTCTGCCCGGAACCATGACT 1020

Qy       1021 TTAGGACTCCTTCAGTTCCTTTAGGACATACTCGCCAAGCCTTGTGCTCACAGGGCAAAG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTAGGACTCCTTCAGTTCCTTTAGGACATACTCGCCAAGCCTTGTGCTCACAGGGCAAAG 1080

Qy       1081 GAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAATGATAAGATTTGATGTTTTTGCTT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAATGATAAGATTTGATGTTTTTGCTT 1140

Qy       1141 GCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTCTGTAGCAGAAAACACGATAAAG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTCTGTAGCAGAAAACACGATAAAG 1200

Qy       1201 CTATGATCTTTATTAGAG 1218
              ||||||||||||||||||
Db       1201 CTATGATCTTTATTAGAG 1218


RESULT 12
US-10-015-393A-5
; Sequence 5, Application US/10015393A
; Publication No. US20030069179A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan 1.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C46
;  CURRENT APPLICATION NUMBER: US/10/015,393A
;  CURRENT FILING DATE:  2002-06-10
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 5
;   LENGTH: 1218
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-015-393A-5

  Query Match            100.0%;  Score 1218;  DB 14;  Length 1218;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1218;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACA 60

Qy         61 AAGGAGTCGCGCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGGAGTCGCGCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGT 120

Qy        121 CAGTGCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CAGTGCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCT 180

Qy        181 GAGGGTTGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGGTTGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACC 240

Qy        241 GGACTGGGGCCGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAAC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGACTGGGGCCGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAAC 300

Qy        301 CTGAGAAACAGCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTGAGAAACAGCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTC 360

Qy        361 CTAGAAGAGGGTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTAGAAGAGGGTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCC 420

Qy        421 CTTCTGAGGAGGCTGCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTTCTGAGGAGGCTGCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCT 480

Qy        481 GTAGTTGATAATGTTGGGAATAAGCTCTGCAACTTTCTTTGGCATTCAGTTGTTAAAAAC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTAGTTGATAATGTTGGGAATAAGCTCTGCAACTTTCTTTGGCATTCAGTTGTTAAAAAC 540

Qy        541 AAATAGGATGCAAATTCCTCAACTCCAGGTTATGAAAACAGTACTTGGAAAACTGAAAAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AAATAGGATGCAAATTCCTCAACTCCAGGTTATGAAAACAGTACTTGGAAAACTGAAAAC 600

Qy        601 TACCTAAATGATCGTCTTTGGTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TACCTAAATGATCGTCTTTGGTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGG 660

Qy        661 TCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTAC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTAC 720

Qy        721 TACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACAC 780

Qy        781 CCAACAGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACACAAGGAGCCAACCACG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CCAACAGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACACAAGGAGCCAACCACG 840

Qy        841 GGACCCTGTTCGGCCACCAAGGAGGGGCCGAGGACCTCATGAGCCAAGGAGAAAGAAACA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGACCCTGTTCGGCCACCAAGGAGGGGCCGAGGACCTCATGAGCCAAGGAGAAAGAAACA 900

Qy        901 AAATGTGGATGGGCTAGTGTTGGACACACTGGCAGTAATACGGACTCTTGTAGATAAGTA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AAATGTGGATGGGCTAGTGTTGGACACACTGGCAGTAATACGGACTCTTGTAGATAAGTA 960

Qy        961 AGTATCTGACTCACGGTCACCTCCAGTGGAATGAAAAGTGTTCTGCCCGGAACCATGACT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGTATCTGACTCACGGTCACCTCCAGTGGAATGAAAAGTGTTCTGCCCGGAACCATGACT 1020

Qy       1021 TTAGGACTCCTTCAGTTCCTTTAGGACATACTCGCCAAGCCTTGTGCTCACAGGGCAAAG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTAGGACTCCTTCAGTTCCTTTAGGACATACTCGCCAAGCCTTGTGCTCACAGGGCAAAG 1080

Qy       1081 GAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAATGATAAGATTTGATGTTTTTGCTT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAATGATAAGATTTGATGTTTTTGCTT 1140

Qy       1141 GCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTCTGTAGCAGAAAACACGATAAAG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTCTGTAGCAGAAAACACGATAAAG 1200

Qy       1201 CTATGATCTTTATTAGAG 1218
              ||||||||||||||||||
Db       1201 CTATGATCTTTATTAGAG 1218
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RESULT 13
US-10-015-869A-5
; Sequence 5, Application US/10015869A
; Publication No. US20030073130A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C45
; CURRENT APPLICATION NUMBER: US/10/015,869A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 5
; LENGTH: 1218
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-015-869A-5

Query Match 100.0%; Score 1218; DB 14; Length 1218;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACA 60

Qy         61 AAGGAGTCGCGCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGGAGTCGCGCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGT 120

Qy        121 CAGTGCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CAGTGCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCT 180

Qy        181 GAGGGTTGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGGTTGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACC 240

Qy        241 GGACTGGGGCCGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAAC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGACTGGGGCCGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAAC 300

Qy        301 CTGAGAAACAGCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTGAGAAACAGCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTC 360

Qy        361 CTAGAAGAGGGTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCC 420
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTAGAAGAGGGTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCC 420

Qy        421 CTTCTGAGGAGGCTGCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTTCTGAGGAGGCTGCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCT 480

Qy        481 GTAGTTGATAATGTTGGGAATAAGCTCTGCAACTTTCTTTGGCATTCAGTTGTTAAAAAC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTAGTTGATAATGTTGGGAATAAGCTCTGCAACTTTCTTTGGCATTCAGTTGTTAAAAAC 540

Qy        541 AAATAGGATGCAAATTCCTCAACTCCAGGTTATGAAAACAGTACTTGGAAAACTGAAAAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AAATAGGATGCAAATTCCTCAACTCCAGGTTATGAAAACAGTACTTGGAAAACTGAAAAC 600

Qy        601 TACCTAAATGATCGTCTTTGGTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TACCTAAATGATCGTCTTTGGTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGG 660

Qy        661 TCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTAC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTAC 720

Qy        721 TACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACAC 780

Qy        781 CCAACAGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACACAAGGAGCCAACCACG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CCAACAGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACACAAGGAGCCAACCACG 840

Qy        841 GGACCCTGTTCGGCCACCAAGGAGGGGCCGAGGACCTCATGAGCCAAGGAGAAAGAAACA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGACCCTGTTCGGCCACCAAGGAGGGGCCGAGGACCTCATGAGCCAAGGAGAAAGAAACA 900

Qy        901 AAATGTGGATGGGCTAGTGTTGGACACACTGGCAGTAATACGGACTCTTGTAGATAAGTA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AAATGTGGATGGGCTAGTGTTGGACACACTGGCAGTAATACGGACTCTTGTAGATAAGTA 960

Qy        961 AGTATCTGACTCACGGTCACCTCCAGTGGAATGAAAAGTGTTCTGCCCGGAACCATGACT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGTATCTGACTCACGGTCACCTCCAGTGGAATGAAAAGTGTTCTGCCCGGAACCATGACT 1020

Qy       1021 TTAGGACTCCTTCAGTTCCTTTAGGACATACTCGCCAAGCCTTGTGCTCACAGGGCAAAG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTAGGACTCCTTCAGTTCCTTTAGGACATACTCGCCAAGCCTTGTGCTCACAGGGCAAAG 1080

Qy       1081 GAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAATGATAAGATTTGATGTTTTTGCTT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAATGATAAGATTTGATGTTTTTGCTT 1140

Qy       1141 GCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTCTGTAGCAGAAAACACGATAAAG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTCTGTAGCAGAAAACACGATAAAG 1200

Qy       1201 CTATGATCTTTATTAGAG 1218
              ||||||||||||||||||
Db       1201 CTATGATCTTTATTAGAG 1218
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RESULT 14
US-10-012-121A-5
; Sequence 5, Application US/10012121A
; Publication No. US20030073810A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C20
; CURRENT APPLICATION NUMBER: US/10/012,121A
; CURRENT FILING DATE: 2001-12-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 5
;   LENGTH: 1218
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-012-121A-5

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  Query Match             100.0%;  Score 1218;  DB 14;  Length 1218;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1218;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACA 60

Qy         61 AAGGAGTCGCGCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGGAGTCGCGCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGT 120

Qy        121 CAGTGCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CAGTGCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCT 180

Qy        181 GAGGGTTGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGGTTGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACC 240

Qy        241 GGACTGGGGCCGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAAC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGACTGGGGCCGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAAC 300

Qy        301 CTGAGAAACAGCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTGAGAAACAGCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTC 360

Qy        361 CTAGAAGAGGGTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTAGAAGAGGGTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCC 420

Qy        421 CTTCTGAGGAGGCTGCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTTCTGAGGAGGCTGCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCT 480

Qy        481 GTAGTTGATAATGTTGGGAATAAGCTCTGCAACTTTCTTTGGCATTCAGTTGTTAAAAAC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTAGTTGATAATGTTGGGAATAAGCTCTGCAACTTTCTTTGGCATTCAGTTGTTAAAAAC 540

Qy        541 AAATAGGATGCAAATTCCTCAACTCCAGGTTATGAAAACAGTACTTGGAAAACTGAAAAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AAATAGGATGCAAATTCCTCAACTCCAGGTTATGAAAACAGTACTTGGAAAACTGAAAAC 600

Qy        601 TACCTAAATGATCGTCTTTGGTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TACCTAAATGATCGTCTTTGGTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGG 660

Qy        661 TCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTAC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTAC 720

Qy        721 TACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        721 TACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACAC 780

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RESULT 15
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; Publication No. US20030082626A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan 1.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C15
; CURRENT APPLICATION NUMBER: US/10/006,116A
; CURRENT FILING DATE: 2001-12-16
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
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; PRIOR FILING DATE: 1998-10-28

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Best Local Similarity 100.0%; Pred. No. 0;
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Job time : 512 secs

GenCore version 5.1.6

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Title: US-10-066-500-8
Perfect score: 1218
Sequence: 1 cccacgcgtccggcgccgtg.....agctatgatctttattagag 1218

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	3	48.6	4.0	7218	1	US-08-232-463-14	Sequence 14, Appl
	4	42.2	3.5	6529	3	US-08-789-329C-1	Sequence 1, Appli
c	5	41.2	3.4	1894	1	US-08-615-170-20	Sequence 20, Appl
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	18	38	3.1	4048	4	US-09-976-594-1053	Sequence 1053, Ap
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ALIGNMENTS

RESULT 1
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; Sequence 3261, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 3261
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 10..213
US-09-621-976-3261

Query Match 26.2%; Score 318.8; DB 4; Length 462;
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Matches 331; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Db      120 AAAACTGCCATTGGATGTCCAGAAATCCCCTGTAGTTGATAATGTTGGGAATAAGCTCTG 179

Qy      510 CAACTTTCTTTGGCATTCAGTTGTTAAAAACAAATAGGATGCAAATTCCTCAACTCCAGG 569
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      180 CAACTTTCTTTGGCATTCAGTTGTTAAAAACAAATAGGATGCAAATTCCTCAACTCCAGG 239

Qy      570 TTATGAAAACAGTACTTGGAAAACTGAAAACTACCTAAATGATCGTCTTTGGTTGGGCCG 629
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      240 TTATGAAAACAGTACTTGGAAAACTGAAAACTACCTAAATGATCGTCTTTGGTTGGGCCG 299

Qy      630 TGTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAGCACATAG 689
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      300 TGTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAGCACATAG 359

Qy      690 CCCACTTCCTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTGCCGAG 749
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      360 CCCACTTCCTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTGCCGAG 419

Qy      750 ATGACAGTGGAACAGATGACAGTGTTGACACCCA 783
            |||||||||||||||||||||||||||||| |
Db      420 ATGACAGTGGAACAGATGACAGTGTTGACACCAA 453
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```
RESULT 2
US-09-086-010-1/c
; Sequence 1, Application US/09086010
; Patent No. 6274338
;  GENERAL INFORMATION:
;    APPLICANT:  Glimcher, Laurie H. et al.
;    TITLE OF INVENTION:  Human c-Maf Compositions and
;    TITLE OF INVENTION:  Methods of Use Thereof
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD, LLP
;      STREET:  28 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/086,010
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/030,579
;      FILING DATE:  2-FEB-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kara, Catherine J.
;      REGISTRATION NUMBER:  41,106
;      REFERENCE/DOCKET NUMBER:  HUI-027CP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)742-4214
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1203 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1203
US-09-086-010-1

  Query Match             4.1%;  Score 49.4;  DB 3;  Length 1203;
  Best Local Similarity   51.6%;  Pred. No. 0.00025;
  Matches  113;  Conservative    0;  Mismatches  106;  Indels    0;  Gaps    0;

Qy          70 CGCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGTCAGTGCCAC 129
               ||||||||||||||||||  |   |  |||||  |  |           ||| |||||
Db         691 CGCCGCCGCCGCCGCCCCCAACGCTGGCCGGGCCACCGCCGCCCGCGCCCCCAGCGCCAC 632

Qy         130 AGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGGTTGG 189
               | ||||    || || |||  | | | ||  |  |  | ||  |  |  ||  ||| |
Db         631 CGGCCGAAGCGGCCGCGCTGCCCGCGGCGCCGGGCGCGCCGGCCGTCGGGTGGTGGTGGT 572

Qy         190 GGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGACTGGGG 249
               || || | | | ||  | ||    |  | | | ||  |    | ||  | |  | | ||
Db         571 GGCCGGCGGCGTGGTGGTGGTGGTGGTAGTGCGGGCCCGCGCCGCTCTGCGCGGCGG 512

Qy         250 CCGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAGGTGGC 288
               ||| ||    | | |    | ||| | |  | |||
Db         511 CCGCGGCGATCACGGCGGACACCACGGCGGCGGCGGGGC 473


RESULT 3
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
;  GENERAL INFORMATION:
;    APPLICANT:  DORNER, F.
;    APPLICANT:  SCHEIFLINGER, F.
;    APPLICANT:  FALKNER, F. G.
;    TITLE OF INVENTION:  RECOMBINANT FOWLPOX VIRUS
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,463
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/935,313
;      FILING DATE:
;      APPLICATION NUMBER:  EP 91 114 300.6
;      FILING DATE:  26-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  30472/114 IMMU
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7218 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      CLONE:  pTZgpt-F1s
US-08-232-463-14

  Query Match             4.0%;  Score 48.6;  DB 1;  Length 7218;
  Best Local Similarity   5.2%;  Pred. No. 0.0011;
  Matches  21;  Conservative  215;  Mismatches  169;  Indels    0;  Gaps    0;

Qy         105 GGGAGGTAGAGAAAGTCAGTGCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCG 164
               :::::: :::::::  :: :  : ::   ::  : : :    :::   ::: : : :
Db        1426 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1367

Qy         165 GAACGGGAGGGAGTCTGAGGGTTGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGC 224
               ::: :::::::::   :::::  ::::: :   : ::::::::::::: ::  :   :::
Db        1366 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1307

Qy         225 CTGGGGCGGGCGGACCGGACTGGGGCCGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAGG 284
                 :::: ::: :::  :::  :::: :::: :::    :::::::   ::::::::::
Db        1306 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1247

Qy         285 TGGCGTTGGTCAGAACCTGAGAAACAGCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAG 344
               :: :  ::  ::::   :::::: ::  ::::::      :  ::::   : :   :::
Db        1246 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1187

Qy         345 GGATCTGAAGAGGTTCCTAGAAGAGGGTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAG 404
               :::   :::::::     :::::::: :          :::::     :  :::::::
Db        1186 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1127

Qy         405 GTTCTTGGGGGTCGCCCTTCTGAGGAGGCTGCGGCTAACAGGGCCCAGAACTGCCATTGG 464
               :    :::::  :       :::::::  : ::  :: :::   ::::  :  :  ::
Db        1126 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1067
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Qy        465 ATGTCCAGAATCCCCTGTAGTTGATAATGTTGGGAATAAGCTCTG 509

Db       1066 ATCGCAAGCTCCCTCGACCTGCAGCCAAGCTCGGAATTAATTCTG 1022


RESULT 4
US-08-789-329C-1
; Sequence 1, Application US/08789329C
; Patent No. 6165755
;  GENERAL INFORMATION:
;    APPLICANT:  SHERWOOD ET AL.
;    TITLE OF INVENTION:  CHICKEN NEUROPEPTIDE GENE USEFUL
;    TITLE OF INVENTION:  FOR IMPROVED POULTRY PRODUCTION
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Klarquist Sparkman Campbell Leigh &
;      ADDRESSEE:  Whinston, LLP
;      STREET:  One World Trade Center
;      STREET:  121 S.W. Salmon Street
;      STREET:  Suite 1600
;      CITY:  Portland
;      STATE:  Oregon
;      COUNTRY:  United States of America
;      ZIP:  97204-2988
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Disk, 3-1/2 inch
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows NT
;      SOFTWARE:  WordPerfect 7.0 & ASCII
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/789,329C
;      FILING DATE:  01/23/97
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Earp, David J.
;      REGISTRATION NUMBER:  41,401
;      REFERENCE/DOCKET NUMBER:  2847-46468/DJE
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (503) 226-7391
;      TELEFAX:  (503) 228-9446
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6529 bp
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-08-789-329C-1

  Query Match              3.5%;  Score 42.2;  DB 3;  Length 6529;
  Best Local Similarity   48.9%;  Pred. No. 0.078;
  Matches  113;  Conservative    0;  Mismatches  118;  Indels    0;  Gaps    0;

Qy          4 ACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACAAAG 63

Db       5433 AGGCGGCCGCACCCGGGGCTCGGCGTCCCTCCCGCGGGGCAGCCCCGGGTGGTGCCATCG 5492

Qy         64 GAGTCGCGCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGTCAG 123

Db       5493 GAGCGAACCCCCCCCGGGAACGCGATGCATAATGCATGGGGGGGGGGGGGGAGACGTCT 5552

Qy        124 TGCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGAGGGAGTCTGAG 183

Db       5553 CGCTCCGGCCCGGCCCCGCCCTTTGTCTGCCGGGAGATGCGGGGCCGGGGCGGGGGTTAG 5612

Qy        184 GGTTGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGG 234

Db       5613 GGCCGGGGTTGGGGTTGGGGTTGGGTTAGGGCCGGGTTGGGTCGGGCCCGG 5663


RESULT 5
US-08-615-170-20/c
; Sequence 20, Application US/08615170
; Patent No. 5776776
;  GENERAL INFORMATION:
;    APPLICANT:  ORDAHL, Charles P.
;    APPLICANT:  AZAKIE, Anthony
;    APPLICANT:  MAR, Janet H.
;    APPLICANT:  FARRANCE, Iain K.G.
;    APPLICANT:  HALL, Deborah E.
;    APPLICANT:  STEWART, Alexandre F.R.
;    APPLICANT:  LARKIN, Sarah B.
;    TITLE OF INVENTION:  DTEF-1 ISOFORMS AND USES THEREOF
;    NUMBER OF SEQUENCES:  32
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  Steuart Street Tower, One Market Plaza
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94105-1493
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/615,170
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/01526
;      FILING DATE:  06-FEB-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/191,493
;      FILING DATE:  04-FEB-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Heslin, James M.
;      REGISTRATION NUMBER:  29,541
;      REFERENCE/DOCKET NUMBER:  2307U-053120
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1894 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-615-170-20

  Query Match              3.4%;  Score 41.2;  DB 1;  Length 1894;
  Best Local Similarity   48.4%;  Pred. No. 0.077;
  Matches  133;  Conservative    3;  Mismatches  137;  Indels    2;  Gaps    1;

Qy         11 CGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACAAAGGAGTCGC 70

Db        475 CTGCTCAATGTCCGGGCTCCACACTCCCTCGGCGTCATTGTCCAGGCTCTTGTCCATCCC 416

Qy         71 GCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGTCAGTGCCACA 130

Db        415 GTCCTGGCCATCTTCCCGCCCCTCCCCGGGGCTGCTGCTGGCGTTCCAGCTGTTGGACGC 356

Qy        131 GCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGAGGGAGTCTGAGGGTTGGG 190

Db        355 TATGGTGCTGGCTGCTCTGGGCTCTGAGCCCGAGCCCCCACGGACACGAGACAACCTGCT 296

Qy        191 GACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGC--GGACCGGACTGGG 248

Db        295 CCGTGCTCCGGAGGGCTGGRCCGKCCACGGGAGCCGGGAGTGGRCCGGGACCGAACCGGG 236
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Qy        249 GCCGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAG 283
Db        235 ACCGGAGCCGGTGCCGGGGATGGNCCGGGGGAGGG 201

RESULT 6
US-08-615-170-18/c
; Sequence 18, Application US/08615170
; Patent No. 5776776
;  GENERAL INFORMATION:
;    APPLICANT:  ORDAHL, Charles P.
;    APPLICANT:  AZAKIE, Anthony
;    APPLICANT:  MAR, Janet H.
;    APPLICANT:  FARRANCE, Iain K.G.
;    APPLICANT:  HALL, Deborah E.
;    APPLICANT:  STEWART, Alexandre F.R.
;    APPLICANT:  LARKIN, Sarah B.
;    TITLE OF INVENTION:  DTEF-1 ISOFORMS AND USES THEREOF
;    NUMBER OF SEQUENCES:  32
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  Steuart Street Tower, One Market Plaza
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94105-1493
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/615,170
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/01526
;      FILING DATE:  06-FEB-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/191,493
;      FILING DATE:  04-FEB-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Heslin, James M.
;      REGISTRATION NUMBER:  29,541
;      REFERENCE/DOCKET NUMBER:  2307U-053120
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1897 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-615-170-18

  Query Match             3.4%;  Score 41.2;  DB 1;  Length 1897;
  Best Local Similarity   48.4%;  Pred. No. 0.077;
  Matches  133;  Conservative    3;  Mismatches  137;  Indels    2;  Gaps    1;

Qy         11 CGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACAAAGGAGTCGC 70
Db        475 CTGCTCAATGTCCGGGCTCCACACTCCCTCGGCGTCATTGTCCAGGCTCTTGTCCATCCC 416

Qy         71 GCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGTCAGTGCCACA 130
Db        415 GTCCTGGCCATCTTCCCGCCCCTCCCCGGGGCTGCTGCTGGCGTTCCAGCTGTTGGACGC 356

Qy        131 GCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGGTTGGG 190
Db        355 TATGGTGCTGGCTGCTCTGGGCTCTGAGCCCGAGCCCCCACGGACACGAGACAACCTGCT 296

Qy        191 GACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGC--GGACCGGACTGGG 248
Db        295 CCGTGCTCCGGAGGGCTGGRCCGKCCACGGGAGCCGGGAGTGGRCCGGGACCGAACCGGG 236

Qy        249 GCCGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAG 283
Db        235 ACCGGAGCCGGTGCCGGGGATGGNCCGGGGGAGGG 201

RESULT 7
US-09-060-756-4
; Sequence 4, Application US/09060756
; Patent No. 6183957
; GENERAL INFORMATION:
;  APPLICANT: Cole, Stewart
;  APPLICANT: Buchrieser-Brosch, Roland
;  APPLICANT: Gordon, Stephen
;  APPLICANT: Billault, Alain
;  TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
;  TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
;  TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
;  FILE REFERENCE: 3495-0169
;  CURRENT APPLICATION NUMBER: US/09/060,756
;  CURRENT FILING DATE: 1998-04-16
;  NUMBER OF SEQ ID NOS: 743
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 1280
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
US-09-060-756-4

  Query Match             3.3%;  Score 40.8;  DB 3;  Length 1280;
  Best Local Similarity   47.0%;  Pred. No. 0.081;
  Matches  126;  Conservative    0;  Mismatches  142;  Indels    0;  Gaps    0;

Qy         38 GCCGTTCTCTCGGACCTGTCACAAAGGAGTCGCGCCGCCGCCGCCGCCCCCTCCCTCCGG 97
Db        523 GGCGGTAGCGCAGGGCTGCTGTTCGGCAGCGGCGGCGCCGGCGGCGCCGGCGGATTTGGT 582

Qy         98 TGGGCCCGGGAGGTAGAGAAAGTCAGTGCCACAGCCCGACCGCGCTGCTCTGAGCCCTGG 157
Db        583 TTCCTCGGTGGGGACGGCGGGGCCGGTGGCAACGCCGGGCTGCTGTTGTCCAGCGGCGGG 642

Qy        158 GCACGCGGAACGGGAGGGAGTCTGAGGGTTGGGGACGTCTGTGAGGGAGGGGAACAGCCG 217
Db        643 GCCGGCGGGTTCGGCGGGTTCGGCACCGCCGGTGGGGTCGGTGGGGCCGGCGGCAATGCC 702

Qy        218 CTCGAGCCTGGGGCGGGCGGACCGGACTGGGGCCGGGGTAGGCTCTGGAAAGGGCCCGGG 277
Db        703 GGCTGGCTGGGCTTCGGCGGGGCCGGGGGCATCGGCGGAATCGGCGGTAACGCTAACGGG 762

Qy        278 AGAGAGGTGGCGTTGGTCAGAACCTGAG 305
Db        763 GGCGCCGGTGGGAACGGCGGCACCGGCG 790

RESULT 8
US-09-670-314-4
; Sequence 4, Application US/09670314
; Patent No. 6492506
; GENERAL INFORMATION:
;  APPLICANT: Cole, Stewart
;  APPLICANT:  Buchrieser-Brosch, Roland
;  APPLICANT:  Gordon, Stephen
;  APPLICANT:  Billault, Alain
;  TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
;  TITLE OF INVENTION:  THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
;  TITLE OF INVENTION:  LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
;  FILE REFERENCE: 3495-0169
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;  CURRENT APPLICATION NUMBER: US/09/670,314
;  CURRENT FILING DATE:  2001-01-12
;  PRIOR APPLICATION NUMBER: 09/060,756
;  PRIOR FILING DATE: 1998-04-16
;  NUMBER OF SEQ ID NOS: 743
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 1280
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
US-09-670-314-4

  Query Match             3.3%;  Score 40.8;  DB 4;  Length 1280;
  Best Local Similarity   47.0%;  Pred. No. 0.081;
  Matches  126;  Conservative    0;  Mismatches  142;  Indels    0;  Gaps    0;

Qy         38 GCCGTTCTCTCGGACCTGTCACAAAGGAGTCGCGCCGCCGCCGCCGCCCCCTCCCTCCGG 97
              | || |  | | |  |||        | ||  ||| ||||| || ||||  |    | |
Db        523 GGCGGTAGCGCAGGGCTGCTGTTCGGCAGCGGCGGCGCCGGCGGCGCCGGCGGATTTGGT 582

Qy         98 TGGGCCCGGGAGGTAGAGAAAGTCAGTGCCACAGCCCGACCGCGCTGCTCTGAGCCCTGG 157
              |    | | | ||  |     | | ||| ||  |||  | | ||  |  ||      | ||
Db        583 TTCCTCGGTGGGGACGGCGGGGCCGGTGGCAACGCCGGGCTGCTGTTGTCCAGCGGCGGG 642

Qy        158 GCACGCGGAACGGGAGGGAGTCTGAGGGTTGGGGACGTCTGTGAGGGAGGGGAACAGCCG 217
              ||  ||||    || |||        |  |  || |  ||| ||| ||  ||| |   | |
Db        643 GCCGGCGGGTTCGGCGGGTTCGGCACCGCCGGTGGGGTCGGTGGGGCCGGCGGCAATGCC 702

Qy        218 CTCGAGCCTGGGGCGGGCGGACCGGACTGGGGCCGGGGTAGGCTCTGGAAAGGGCCCGGG 277
                |  ||  ||   |||||  | |   |  | | || |    | | || |    ||||
Db        703 GGCTGGCTGGGCTTCGGCGGGGCCGGGGGCATCGGCGGAATCGGCGGTAACGCTAACGGG 762

Qy        278 AGAGAGGTGGCGTTGGTCAGAACCTGAG 305
              | |  |  | |   | | | ||| | |
Db        763 GGCGCCGGTGGGAACGGCGGCACCGGCG 790


RESULT 9
US-09-165-264-11
; Sequence 11, Application US/09165264
; Patent No. 6197510
; GENERAL INFORMATION:
;  APPLICANT:  Vinayagamoorthy, Thuraiayah
;  TITLE OF INVENTION:  Multi-Loci Genomic Analysis
;  FILE REFERENCE:  44747
;  CURRENT APPLICATION NUMBER: US/09/165,264
;  CURRENT FILING DATE:  1998-10-01
;  NUMBER OF SEQ ID NOS:  14
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 11
;   LENGTH: 320
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Primer sequence
US-09-165-264-11

  Query Match             3.2%;  Score 39.4;  DB 3;  Length 320;
  Best Local Similarity   53.6%;  Pred. No. 0.097;
  Matches   82;  Conservative    0;  Mismatches   71;  Indels    0;  Gaps    0;

Qy        156 GGGCACGCGGAACGGGAGGGAGTCTGAGGGTTGGGGACGTCTGTGAGGGAGGGGAACAGC 215
              |||   | ||   ||| ||| |   | |||  ||||  |   | | ||| ||||    |
Db        163 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 222

Qy        216 CGCTCGAGCCTGGGGCGGGCGGACCGGACTGGGGCCGGGGTAGGCTCTGGAAAGGGCCCG 275
              |   | |   |||| ||| ||   ||   ||||  |||| ||    ||   |||   |
Db        223 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 282

Qy        276 GGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAA 308
              || | | || || |  || ||||   |||  ||
Db        283 GGGGGGGGGGGGGGGGGGGCAGATTTTGAAGAA 315


RESULT 10
US-09-866-108A-15742/c
; Sequence 15742, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108A
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 15755
;  SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 15742
;   LENGTH: 500
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108A-15742

  Query Match             3.2%;  Score 39.4;  DB 4;  Length 500;
  Best Local Similarity   49.3%;  Pred. No. 0.12;
  Matches  103;  Conservative    0;  Mismatches  106;  Indels    0;  Gaps    0;

Qy         63 GGAGTCGCGCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGTCA 122
              ||  || | | ||  | || |  ||   |   |||||    | || | | ||||| | |
Db        220 GGCTTCACTCTGCTCCAGCTGGACCAGGCAAGAGGTGGAGAAGAGAAGAAAAGAAAATGA 161

Qy        123 GTGCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCTGA 182
              |      ||   | | |   |||   ||| | | || | |||||||    ||
Db        160 GAAGGGAAGAGGGGAAGGGAGGTGGGGAGGGGAGGGAAGGTGGGAGGGGAGGGGAGGTGG 101

Qy        183 GGGTTGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGG 242
              | |  | ||     || ||||| ||| | |  | | |      | || |||  ||  |
Db        100 GAGGGGAGGGGAGGTGGGAGGGGAGGGGAGGGGAGGTGGGAGGGGAGGGGGGAAGAGAGC 41

Qy        243 ACTGGGGCCGGGGTAGGCTCTGGAAAGGG 271
                 ||||  |||  |||    || | | |
Db         40 GGAGGGGAAGGGAGAGGGGAGGGGAGGCG 12


RESULT 11
US-09-754-250-3
; Sequence 3, Application US/09754250
; Patent No. 6376225
; GENERAL INFORMATION:
```

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;  APPLICANT: WEI, Ming-Hui et al
;  TITLE OF INVENTION: ISOLATED HUMAN PHOSPHODIESTERASE
;  TITLE OF INVENTION:  PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
;  TITLE OF INVENTION:  PHOSPHODIESTERASE PROTEINS, AND USES THEREOF
;  FILE REFERENCE: CL001063
;  CURRENT APPLICATION NUMBER: US/09/754,250
;  CURRENT FILING DATE:  2001-01-05
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 111282
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(111282)
;   OTHER INFORMATION: n = A,T,C or G
US-09-754-250-3

  Query Match             3.2%;  Score 39.2;  DB 4;  Length 111282;
  Best Local Similarity   50.5%;  Pred. No. 2.7;
  Matches   95;  Conservative    0;  Mismatches   93;  Indels    0;  Gaps    0;

Qy        102 CCCGGGAGGTAGAGAAAGTCAGTGCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCAC 161
              || ||| |  | ||||     ||| ||  | |||   |  | |     |       |  |
Db      39453 CCAGGGCGAGACAGAAGCGGGGTGACAGCGGCCGGGTGTCCGGTGGGGTCGGAGGATCCG 39512

Qy        162 GCGGAACGGGAGGGAGTCTGAGGGTTGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCG 221
              ||| || ||||      | | | ||| | | |   | || | |     |     | | |
Db      39513 ACGGGCCGAGAGGTGCGGTCCGCGGTGGCGGGGACATAGGCGGGGCCGGGGCGGGCCGGG 39572

Qy        222 AGCCTGGGGCGGGCGGACCGGACTGGGGCCGGGGTAGGCTCTGGAAAGGGCCCGGGAGAG 281
              ||  | || ||||||| ||||   ||||||||||  | | || |   || || ||   ||
Db      39573 GGCGGGCGGGGGGCGGGCCGGGGCGGGGCCGGGGCGGACACTCGGGCGGACCAGGCGAAG 39632

Qy        282 AGGTGGCG 289
                || |||
Db      39633 CTGTCGCG 39640


RESULT 12
US-09-252-991A-5281/c
; Sequence 5281, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 5281
;   LENGTH: 723
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5281

  Query Match             3.2%;  Score 39;  DB 4;  Length 723;
  Best Local Similarity   47.1%;  Pred. No. 0.2;
  Matches  120;  Conservative    0;  Mismatches  135;  Indels    0;  Gaps    0;

Qy          8 GTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACAAAGGAGT 67
              | ||   | ||  |||  ||| ||  |    |    | || ||||||  |    |   || |
Db        571 GCCCCAGGGCGCCGCCAGGCGGCCCGCGGCGAGATCGTCGCGGACCAGCGCCTCCGGGGC 512

Qy         68 CGCGCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGTCAGTGCC 127
                | |  |||||  |||| |  || ||| |     | ||  |||||||    ||    ||
Db        511 GATGGCCACGCCGAGGCCCGCCACCGCCGCTTCCAGCAGGTAGTAGAGATGCTCGAACCC 452

Qy        128 ACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGGTT 187
              |||  | |||   ||      | | | | |  |     ||     | | |   |
Db        451 CTGGCCATAGCGCAGCGCCTCCGCCGCCAGCCCCTGGCTCGCGGCCCAGGCCGGCCAGGC 392

Qy        188 GGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGACTGG 247
              ||      | |  ||   | | |||| ||||  ||    | || ||||   |  | |
Db        391 CTGGGGTCGCGAGGCGGTATGCAGCAGCGGCTCCTGCAACAGCCGCGCGGCGGGCGCCTG 332

Qy        248 GGCCGGGGTAGGCTC 262
              |||| ||   |  ||
Db        331 GGCCAGGCCGGTTTC 317


RESULT 13
US-09-252-991A-5345/c
; Sequence 5345, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 5345
;   LENGTH: 744
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5345

  Query Match             3.2%;  Score 39;  DB 4;  Length 744;
  Best Local Similarity   47.1%;  Pred. No. 0.2;
  Matches  120;  Conservative    0;  Mismatches  135;  Indels    0;  Gaps    0;

Qy          8 GTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACAAAGGAGT 67
              | ||   | ||  |||  ||| ||  |    |    | || ||||||  |    |   || |
Db        602 GCCCCAGGGCGCCGCCAGGCGGCCCGCGGCGAGATCGTCGCGGACCAGCGCCTCCGGGGC 543

Qy         68 CGCGCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGTCAGTGCC 127
                | |  |||| |  || ||| |     | ||  |||||||    ||    ||
Db        542 GATGGCCACGCCGAGGCCCGCCACCGCCGCTTCCAGCAGGTAGTAGAGATGCTCGAACCC 483

Qy        128 ACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGGTT 187
              |||  | |||   ||      | | | | |  |     ||     | | |   |
Db        482 CTGGCCATAGCGCAGCGCCTCCGCCGCCAGCCCCTGGCTCGCGGCCCAGGCCGGCCAGGC 423

Qy        188 GGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGACTGG 247
              ||      | |  ||   | | |||| ||||  ||    | || ||||   |  | |
Db        422 CTGGGGTCGCGAGGCGGTATGCAGCAGCGGCTCCTGCAACAGCCGCGCGGCGGGCGCCTG 363

Qy        248 GGCCGGGGTAGGCTC 262
              |||| ||   |  ||
Db        362 GGCCAGGCCGGTTTC 348


RESULT 14
US-09-252-991A-5307/c
; Sequence 5307, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
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;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 5307
;   LENGTH: 954
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5307

  Query Match             3.2%;  Score 39;  DB 4;  Length 954;
  Best Local Similarity   47.1%;  Pred. No. 0.23;
  Matches  120;  Conservative    0;  Mismatches  135;  Indels    0;  Gaps    0;

Qy          8 GTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACAAAGGAGT 67
              | ||   | ||  |||  ||| ||  |   |   |  || ||||||  |   |  || |
Db        849 GCCCCAGGGCGCCGCCAGGCGGCCCGCGGCGAGATCGTCGCGGACCAGCGCCTCCGGGGC 790

Qy         68 CGCGCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGTCAGTGCC 127
                | |  |||||  |||| |  || ||| |     | ||  |||||||   ||    ||
Db        789 GATGGCCACGCCGAGGCCCGCCACCGCCGCTTCCAGCAGGTAGTAGAGATGCTCGAACCC 730

Qy        128 ACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGGTT 187
                |||  | |||  ||       | |  | | |  |    ||     | | |   |
Db        729 CTGGCCATAGCGCAGCGCCTCCGCCGCCAGCCCCTGGCTCGCGGCCCAGGCCGGCCAGGC 670

Qy        188 GGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGACTGG 247
                ||      | |  ||   | | |||| |||| ||    | || ||||  |  |   |
Db        669 CTGGGGTCGCGAGGCGGTATGCAGCAGCGGCTCCTGCAACAGCCGCGCGGCGGGCGCCTG 610

Qy        248 GGCCGGGGTAGGCTC 262
              |||| ||   |  ||
Db        609 GGCCAGGCCGGTTTC 595


RESULT 15
US-09-292-034-1
; Sequence 1, Application US/09292034
; Patent No. 6492343
; GENERAL INFORMATION:
;  APPLICANT: Reddy, P. Seshidhar
;  APPLICANT: Tikoo, Suresh
;  APPLICANT: Babiuk, Lorne
;  TITLE OF INVENTION: PORCINE ADENOVIRUS TYPE 3 GENOME
;  FILE REFERENCE: 293102002400
;  CURRENT APPLICATION NUMBER: US/09/292,034
;  CURRENT FILING DATE: 1999-04-14
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 34094
;   TYPE: DNA
;   ORGANISM: Porcine Adenovirus Type 3
;   FEATURE:
US-09-292-034-1

  Query Match             3.2%;  Score 38.4;  DB 4;  Length 34094;
  Best Local Similarity   54.2%;  Pred. No. 2.4;
  Matches   78;  Conservative    0;  Mismatches   66;  Indels    0;  Gaps    0;

Qy         34 CTTTGCCGTTCTCTCGGACCTGTCACAAAGGAGTCGCGCCGCCGCCGCCGCCCCCTCCCT 93
              || |||||    | |     |   | | |  | | |   ||  || || |||||  |  | |
Db      31399 CTCTGCCGGGACCACCACTCCCCCTCCGTGAACTGCTGCTTCCTCCCCCGCCGCTGCGCC 31458

Qy         94 CCGGTGGGCCCGGGAGGTAGAGAAAGTCAGTGCCACAGCCCGACCGCGCTGCTCTGAGCC 153
              ||| ||| | | |  |  ||    || ||||||| ||  |     |||| || | |||||
Db      31459 CCGATGGCCTCCGCCGCCAGCTTCAGCCAGTGCCGCAAGCGCTGGGCGCAGCGCCGAGCC 31518

Qy        154 CTGGGCACGCGGAACGGGAGGGAG 177
                |||  |||  | |  | || ||
Db      31519 ACCGGCTCGCTCAGCTCGTGGCAG 31542
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Search completed: April  4, 2004, 09:02:45
Job time : 131 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 4, 2004, 05:01:37 ; Search time 3064 Seconds
(without alignments)
11870.802 Million cell updates/sec

Title: US-10-066-500-8
Perfect score: 1218
Sequence: 1 cccacgcgtccggcgccgtg.....agctatgatctttattagag 1218

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	727	59.7	801	12	BG772050	BG772050 602721686
	2	688	56.5	781	14	CD109369	CD109369 AGENCOURT
	3	686.8	56.4	701	14	CB295705	CB295705 12B22056_
c	4	683.2	56.1	760	13	BQ576035	BQ576035 UI-H-EZ1-
	5	602.8	49.5	3391	11	AK032416	AK032416 Mus muscu
	6	582.8	47.8	591	14	CB295706	CB295706 12B22056_
	7	550.4	45.2	892	13	BU152634	BU152634 AGENCOURT
	8	535.4	44.0	722	12	BG744401	BG744401 602723139
	9	505.4	41.5	711	12	BI666950	BI666950 603291808
	10	505.4	41.5	835	13	BU161287	BU161287 AGENCOURT
	11	505.4	41.5	857	13	BU500574	BU500574 AGENCOURT
	12	505.4	41.5	871	13	BQ439291	BQ439291 AGENCOURT
	13	503.8	41.4	670	14	CD683922	CD683922 EST442 hu
	14	503.8	41.4	727	12	BG749354	BG749354 602707829
	15	503.8	41.4	834	12	BI668768	BI668768 603294714
	16	499.4	41.0	588	13	BU072529	BU072529 im44d03.y
	17	498	40.9	1821	11	AK043522	AK043522 Mus muscu
	18	493.4	40.5	692	12	BG699229	BG699229 602678896
	19	483.2	39.7	700	9	AU253442	AU253442 AU253442
	20	482.8	39.6	611	14	CD690289	CD690289 EST6812 h
	21	478.6	39.3	899	10	BF797383	BF797383 602257026
	22	478.2	39.3	742	10	BE882864	BE882864 601509268
	23	477.8	39.2	908	14	CA978792	CA978792 AGENCOURT
	24	477.6	39.2	623	13	BX482659	BX482659 DKFZp686O
	25	464.6	38.1	789	12	BG620045	BG620045 602618260
	26	456.8	37.5	921	12	BM010902	BM010902 603634540
	27	440.4	36.2	556	12	BG773383	BG773383 602722169
	28	436.8	35.9	962	14	CB183456	CB183456 AGENCOURT
	29	434.4	35.7	579	14	CD691874	CD691874 EST8429 h
	30	430.8	35.4	560	9	AL703545	AL703545 DKFZp686D
	31	428.4	35.2	531	12	BG719220	BG719220 602690279
	32	421.6	34.6	893	13	BQ899613	BQ899613 AGENCOURT
	33	405.6	33.3	745	12	BI768690	BI768690 603057251
	34	397.8	32.7	518	14	CA392843	CA392843 cs29e09.y
	35	388.2	31.9	936	10	BF781079	BF781079 602106720
	36	387.2	31.8	1999	11	AK076799	AK076799 Mus muscu
	37	384.8	31.6	629	13	BY729431	BY729431 BY729431
	38	382	31.4	510	29	CG542955	CG542955 OST138142
	39	380.2	31.2	420	13	BX487789	BX487789 DKFZp686B
c	40	380	31.2	394	10	AW296811	AW296811 UI-H-BW0-
	41	376.4	30.9	405	9	AA373599	AA373599 EST85637
	42	366	30.0	819	9	AU080966	AU080966 AU080966
c	43	365.6	30.0	475	13	BX529453	BX529453 BX529453
	44	360.2	29.6	488	29	CG608250	CG608250 OST288186
	45	352	28.9	723	12	BG165215	BG165215 602344087

ALIGNMENTS

RESULT 1
BG772050
LOCUS BG772050 801 bp mRNA linear EST 15-MAY-2001
DEFINITION 602721686F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4838565 5', mRNA sequence.
ACCESSION BG772050
VERSION BG772050.1 GI:14082703
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 801)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10772 row: 1 column: 22

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          High quality sequence stop: 787.
FEATURES             Location/Qualifiers
     source          1. .801
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4838565"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_97"
                     /note="Organ: testis; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
                     (gtcgag); Oligo-dT primed using primer
                     5'-TTTTTTTTTTTTTTTTVN-3', size-selected for average
                     insert size 2.2 kb and normalized to ROT 5. This is a
                     primary library enriched for full-length clones and
                     constructed using the Cap-trapper method (Carninci, in
                     preparation). Library constructed by M. Brownstein
                     (NIMH/NHGRI, National Institutes of Health). Note: this is
                     a NIH_MGC Library."
ORIGIN

  Query Match             59.7%;  Score 727;  DB 12;  Length 801;
  Best Local Similarity   98.7%;  Pred. No. 2.4e-174;
  Matches  764;  Conservative    0;  Mismatches    6;  Indels    4;  Gaps    3;

Qy        184 GGTTGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGA 243
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 GGTAGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGA 63

Qy        244 CTGGGGCCGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAACCTG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 CTGGGGCCGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAACCTG 123

Qy        304 AGAAACAGCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCCTA 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 AGAAACAGCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCCTA 183

Qy        364 GAAGAGGGTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCCCTT 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GAAGAGGGTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCCCTT 243

Qy        424 CTGAGGAGGCTGCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCTGTA 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 CTGAGGAGGCTGCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCTGTA 303

Qy        484 GTTGATAATGTTGGGAATAAGCTCTGCAACTTTCTTTGGCATTCAGTTGTTAAAAACAAA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 GTTGATAATGTTGGGAATAAGCTCTGCAACTTTCTTTGGCATTCAGTTGTTAAAAACAAA 363

Qy        544 TAGGATGCAAATTCCTCAACTCCAGGTTATGAAAACAGTACTTGGAAAACTGAAAACTAC 603
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TAGGATGCAAATTCCTCAACTCCAGGTTATGAAAACAGTACTTGGAAAACTGAAAACTAC 423

Qy        604 CTAAATGATCGTCTTTGGTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCT 663
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 CTAAATGATCGTCTTTGGTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCT 483

Qy        664 GTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTACTAC 723
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 GTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTACTAC 543

Qy        724 CATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACACCCA 783
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        544 CATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTNGACACCCA 603

Qy        784 ACAGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACACAAGGAGCCAACCACGGGA 843
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 ACAGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACACAAGGAGCCAACCACGGGA 663

Qy        844 CCCTGTTCGGCCACCAAGGAGGGGCCGAGGACCTCATGAGCCAAGGAGAAAGAAACAAAA 903
              ||||||||||   | | ||||||||||||||||||||||||||||||||||| |||
Db        664 CCCTGTTCGGC--ACCAAGAGGGGCCGAGGACCTCATGAGCCAAGGAGAAAGAAAC-AAA 720

Qy        904 TGTGGATGGGCTAGTGTTGGACACACTGGCAGTAATACGGACTCTTGTAGATAA 957
              |||||||||||||||||||||||||||||||||||| |||||||||||||| ||||
Db        721 TGTGGATGGGCTAGTGTTGGACACACTGGCAGT-ATACGGACTCTTGTTGATAA 773


RESULT 2
CD109369
LOCUS       CD109369                781 bp    mRNA    linear   EST 15-MAY-2003
DEFINITION  AGENCOURT_13988396 NIH_MGC_147 Homo sapiens cDNA clone
            IMAGE:30346743 5', mRNA sequence.
ACCESSION   CD109369
VERSION     CD109369.1  GI:30753482
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 781)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Stefan Hansson
             cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
            and advice from Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDAM386  row: 1  column: 16
            High quality sequence stop: 613.
FEATURES             Location/Qualifiers
     source          1. .781
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:30346743"
                     /tissue_type="Human Placenta"
                     /lab_host="DH10B TonA"
                     /clone_lib="NIH_MGC_147"
                     /note="Organ: placenta; Vector: pBluescriptR; Site_1:
                     alI-XhoI; Site_2: BamH; Oligo-dT primed using primer
                     5'-TTTTTTTTTTTTTTTTVN-3', size-selected for average
                     insert size 2.3 kb and normalized to ROT 5. This is a
                     primary library enriched for full-length clones and
                     constructed using the Cap-trapper method (Carninci, in
                     preparation). Library constructed by M. Brownstein
                     (NIMH/NHGRI, National Institutes of Health). Note: This is
                     a NIH_MGC library."
ORIGIN

  Query Match             56.5%;  Score 688;  DB 14;  Length 781;
  Best Local Similarity   98.8%;  Pred. No. 2.1e-164;
  Matches  735;  Conservative    0;  Mismatches    5;  Indels    4;  Gaps    4;

Qy         57 CACAAAGGAGTCGCGCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGA 116
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         25 CAGAAAGGAGTCGCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGA 84

Qy        117 AAGTCAGTGCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGA 176
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 AAGTCAGTGCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGA 144

Qy        177 GTCTGAGGGTTGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCG 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 GTCTGAGGGTTGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCG 204

Qy        237 GACCGGACTGGGGCCGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCA 296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GACCGGACTGGGGCCGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCA 264
```

```
Qy        297 GAACCTGAGAAACAGCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAG 356
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 GAACCTGAGAAACAGCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAG 324

Qy        357 GTTCCTAGAAGAGGGTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGT 416
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 GTTCCTAGAAGAGGGTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGT 384

Qy        417 CGCCCTTCTGAGGAGGCTGCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATC 476
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CGCCCTTCTGAGGAGGCTGCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATC 444

Qy        477 CCCTGTAGTTGATAATGTTGGGAATAAGCTCTGCAACTTTCTTTGGCATTCAGTTGTTAA 536
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 CCCTGTAGTTGATAATGTTGGGAATAAGCTCTGCAACTTTCTTTGGCATTCAGTTGTTAA 504

Qy        537 AAACAAATAGGATGCAAATTCCTCAACTCCAGGTTATGAAAACAGTACTTGGAAAACTGA 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 AAACAAATAGGATGCAAATTCCTCAACTCCAGGTTATGAAAACAGTACTTGGAAAACTGA 564

Qy        597 AAACTACCTAAATGATCGTCTTTGGTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCC 656
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 AAACTACCTAAATGATCGTCTTTGGTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCC 624

Qy        657 AGGGTCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGACTGGAGGTG-CC 715
              ||||||||||||||||||||||||||||||||||||||||||  |||||||  ||| ||
Db        625 AGGGTCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTTAGGACTGGGAGTGCCC 684

Qy        716 GCTACTACCAT-GGGTAATTCCTGTATCTG-CCGAGATGACAGTGGAACAGATGACAGTG 773
              |||||||||| |||||||||||||||||| |||||||||||||||||||||||||||||||
Db        685 GCTACTACCATGGGGTAATTCCTGTATCTGCCCGAGATGACAGTGGAACAGATGACAGTG 744

Qy        774 -TTGACACCCAACAGCAACAGGCC 796
               |||||||||||||||||||||||
Db        745 TTTGACACCCAACAGCAACAGGCC 768
```

RESULT 3
CB295705

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LOCUS       CB295705                701 bp    mRNA    linear   EST 28-FEB-2003
DEFINITION  12B22056_rev_1_E02_r_007.ab1 Chimpanzee brain library Koos Pan
            troglodytes cDNA clone 12B22056_rev_1_E02_r_007.ab1 5', mRNA
            sequence.
ACCESSION   CB295705
VERSION     CB295705.1  GI:28621135
KEYWORDS    EST.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1  (bases 1 to 701)
  AUTHORS   Hellmann,I., Zollner,S., Enard,W., Ebersberger,I., Nickel,B. and
            Paabo,S.
  TITLE     Selection on human genes as revealed by comparisons to chimpanzee
            cDNA
  JOURNAL   Genome Res. (2003) In press
COMMENT     Contact: Paabo S
            Evolutionary Genetics
            Max-Planck-Institute for evolutionary Anthropology
            Deutscher Platz 6, 04103 Leipzig, Germany
            Tel: +49-(0)-341-3550 500
            Fax: +49-(0)-341-3550 555
            Email: paabo@eva.mpg.de
            Seq primer: M13 reverse.
FEATURES             Location/Qualifiers
     source          1. .701
                     /organism="Pan troglodytes"
                     /mol_type="mRNA"
                     /db_xref="taxon:9598"
                     /clone="12B22056_rev_1_E02_r_007.ab1"
                     /sex="male"
                     /tissue_type="brain, presumably cortex"
                     /dev_stage="adult"
                     /lab_host="Epicurian Coli (TM) XL-10-Gold"
                     /clone_lib="Chimpanzee brain library Koos"
                     /note="Vector: pUChi; Site_1: SfiI-A; Site_2: SfiI-B; The
                     library was prepared using the SMART cDNA library
                     construction Kit (Clontech), doing only primer extension,
                     but not PCR amplification of the cDNA. The only deviation
                     from the published protocoll was that we cloned the cDNA
                     into a plasmid Vector."
ORIGIN
```

```
  Query Match           56.4%;  Score 686.8;  DB 14;  Length 701;
  Best Local Similarity   98.7%;  Pred. No. 4.1e-164;
  Matches  688;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy        261 TCTGGAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACAGCCGAGAGGT 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TCTGGAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACAGCCGAGAGGT 60

Qy        321 TTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCCTAGAAGAGGGTGTTCCCTC 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCCTAGAAGAGGGTGTTCCCTC 120

Qy        381 TTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCCCTTCTGAGGAGGCTGCGGCT 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCCCTTCTGAGGAGGCTGCGGCT 180

Qy        441 AACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCTGTAGTTGATAATGTTGGGAA 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCTGTAGTTGATAATGTTGGGAA 240

Qy        501 TAAGCTCTGCAACTTTCTTTGGCATTCAGTTGTTAAAAACAAATAGGATGCAAATTCCTC 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TAAGCTCTGCAACTTTCTTTGGCATTCAGTTGTTAAAAACAAATAGGATGCAAATTCCTC 300

Qy        561 AACTCCAGGTTATGAAAACAGTACTTGGAAAACTGAAAACTACCTAAATGATCGTCTTTG 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AACTCCAGGTTATGAAAACAGTACTTGGAAAACTGAAAACTACCTAAATGATCGTCTTTG 360

Qy        621 GTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAG 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAG 420

Qy        681 AGCACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTA 740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGCACATAGCCCACTTCCTAGGGACTGGAGGTGCTGCTACTACCATGGGTAATTCCTGTA 480

Qy        741 TCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACACCCAACAGCAACAGGCCGAGA 800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACACCCAACAGCAACAGGCCGAGA 540

Qy        801 ACAGTGCAGTACCCACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTCGGCCACCAA 860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db        541 ACAGTGCAGTACCCACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTCGGCNACCAA 600

Qy        861 GGAGGGGCCGAGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGT 920
              |||||||||||||||| |||||||||| |||||||||||||| ||||||||||||||||||
Db        601 GGAGGGGCCGAGGACCGCATGAGCCAANGAGAAAGAAACAAANTGTGGATGGGCTAGTGT 660

Qy        921 TGGACACACTGGCAGTAATACGGACTCTTGTAGATAA 957
              || |||||||||||||||||||||||||||| | | |
Db        661 TGNACACACTGGCAGTAATACGGACTCTTGTNGNTNA 697
```

RESULT 4
BQ576035/c

```
LOCUS       BQ576035                760 bp    mRNA    linear   EST 19-JUN-2002
DEFINITION  UI-H-EZ1-bbg-c-03-0-UI.s1 NCI_CGAP_Ch2 Homo sapiens cDNA clone
            UI-H-EZ1-bbg-c-03-0-UI 3', mRNA sequence.
ACCESSION   BQ576035
VERSION     BQ576035.1  GI:21479352
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
```

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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 760)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian, Dept. of
            Orthoapedics
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .760
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-EZ1-bbg-c-03-0-UI"
                     /tissue_type="Chondrosarcoma Grade II"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_Ch2"
                     /note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
                     with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_Ch2 is a normalized cDNA library containing the
                     following tissue(s): Chondrosarcoma Grade II. The library
                     was constructed according to Bonaldo, Lennon and Soares,
                     Genome Research, 6:791-806, 1996. First strand cDNA
                     synthesis was primed with an oligo-dT primer containing a
                     Not I site. Double stranded cDNA was ligated to an EcoR I
                     adaptor, digested with Not I, and cloned directionally
                     into pT7T3-Pac vector. The oligonucleotide used to prime
                     the synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     TGATCACGCT.
                     TAG_TISSUE=grade-2-chondrosarcoma
                     TAG_LIB=UI-H-EZ1
                     TAG_SEQ=ATCTAATATG"
ORIGIN

  Query Match           56.1%;  Score 683.2;  DB 13;  Length 760;
  Best Local Similarity  98.9%;  Pred. No. 3.5e-163;
  Matches  696;  Conservative    0;  Mismatches    7;  Indels    1;  Gaps    1;

Qy        515 TTCTTTGGCATTCAGTTGTTAAAAACAAATAGGATGCAAATTCCTCAACTCCAGGTTATG 574
              ||  |||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db        721 TTTCTTGGCATTCAGTTGTTAAAAACAAATAGGATGC-AATTCCTCAACTCCAGGTTATG 663

Qy        575 AAAACAGTACTTGGAAAACTGAAAACTACCTAAATGATCGTCTTTGGTTGGGCCGTGTTC 634
              ||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db        662 AAAACAGTACTTGGAAAACTGAAAACTACCTAAATGATTGTCTTTGGTTGGGCCGTGTTC 603

Qy        635 TTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAGCACATAGCCCAC 694
              |||||||||||||||||||||||||||||||||||||| | ||||||||||||||||||
Db        602 TTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTNTNGAAGAGCACATAGCCCAC 543

Qy        695 TTCCTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTGCCGAGATGAC 754
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db        542 TTCCTAGGGACTGGAGGTGCCGCTANTACCATGGGTAATTCCTGTATCTGCCGAGATGAC 483

Qy        755 AGTGGAACAGATGACAGTGTTGACACCCAACAGCAACAGGCCGAGAACAGTGCAGTACCC 814
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 AGTGGAACAGATGACAGTGTTGACACCCAACAGCAACAGGCCGAGAACAGTGCAGTACCC 423

Qy        815 ACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTCGGCCACCAAGGAGGGGCCGAGGA 874
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        422 ACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTCGGCCACCAAGGAGGGGCCGAGGA 363

Qy        875 CCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTTGGACACACTGGCA 934
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 CCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTTGGACACACTGGCA 303

Qy        935 GTAATACGGACTCTTGTAGATAAGTAAGTATCTGACTCACGGTCACCTCCAGTGGAATGA 994
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        302 GTAATACGGACTCTTGTAGATAAGTAAGTATNTGACTCACGGTCACCTCCAGTGGAATGA 243

Qy        995 AAAGTGTTCTGCCCGGAACCATGACTTTAGGACTCCTTCAGTTCCTTTAGGACATACTCG 1054
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 AAAGTGTTCTGCCCGGAACCATGACTTTAGGACTCCTTCAGTTCCTTTAGGACATACTCG 183

Qy       1055 CCAAGCCTTGTGCTCACAGGGCAAAGGAGAATATTTTAATGCTCCGCTGATGGCAGAGTA 1114
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CCAAGCCTTGTGCTCACAGGGCAAAGGAGAATATTTTAATGCTCCGCTGATGGCAGAGTA 123

Qy       1115 AATGATAAGATTTGATGTTTTTGCTTGCTGTCATCTACTTTGTCTGGAAATGTCTAAATG 1174
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 AATGATAAGATTTGATGTTTTTGCTTGCTGTCATCTACTTTGTCTGGAAATGTCTAAATG 63

Qy       1175 TTTCTGTAGCAGAAAACACGATAAAGCTATGATCTTTATTAGAG 1218
              |||||||||||||||||||||||||||||||||||||||||||
Db          62 TTTCTGTAGCAGAAAACACGATAAAGCTATGATCTTTATTAGAG 19


RESULT 5
AK032416
LOCUS       AK032416               3391 bp    mRNA    linear   HTC 18-SEP-2003
DEFINITION  Mus musculus adult male olfactory brain cDNA, RIKEN full-length
            enriched library, clone:6430540K08 product:hypothetical SPla and
            the RYanodine Receptor (SPRY)/SPRY domain/RING finger containing
            protein, full insert sequence.
ACCESSION   AK032416
VERSION     AK032416.1  GI:26328234
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
```

```
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 3391)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.go.jp/
            URL:http://fantom.gsc.riken.go.jp/.
FEATURES             Location/Qualifiers
     source          1. .3391
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                     /mol_type="mRNA"
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                     /db_xref="MGI:2395918"
                     /db_xref="taxon:10090"
                     /clone="6430540K08"
                     /sex="male"
                     /tissue_type="olfactory brain"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="adult"
     CDS             606. .2336
                     /note="unnamed protein product; hypothetical SPla and the
                     RYanodine Receptor (SPRY)/SPRY domain/RING finger
                     containing protein (InterPro|IPR003877,
                     InterPro|IPR003878, InterPro|IPR001841, evidence:
                     InterPro)
                     putative"
                     /codon_start=1
                     /protein_id="BAC27858.1"
                     /db_xref="GI:26328235"
                     /translation="MIVFGWAVFLASRSLGQGLLLTLEEHIAHLLGTTGATATMGNSC
                     ICRDDSGAEDNVDTHQQQAENSTVPTADSRSQPRDPVRPPRRGRGPHEPRRKKQNVDG
                     LVLDTLAVIRTLVDNDQEPPYSMITLHEMAETDEGWLDVVQSLIRVIPLEDPLGPAVI
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                     IGLLSPGILEYLLQCLKLQSHPTVMLFALIAMEKFAQTSENKLTISESSISDRLVTLE
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                     PHGLEARCDASSFESVRCTFCVDTGVWYYEVTVVTSGVMQIGWATRDSKFLNHEGYGI
                     GDDEYSCAYDGCRQLIWYNARSKPHVHPCWKEGDTVGFLLDLNEKQMIFFLNGNQLPP
                     EKQVFSSTVSGFFAAASFMSYQQCEFNFGARPFKYPPSMKFSTFNDYAFLTAEEKIIL
                     PRHRRLALLKQVSIRENCCSLCCDEVADTQLKPCGHSDLCMDCALQLETCPLCRKEIV
                     SRIRQISHIS"
ORIGIN

  Query Match           49.5%;  Score 602.8;  DB 11;  Length 3391;
  Best Local Similarity 80.3%;  Pred. No. 2.1e-142;
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  Matches  764;  Conservative    0;  Mismatches  167;  Indels   21;  Gaps    4;

Qy       11 CGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACAAAGGAGTCGC 70
Db       20 CAGTGCCGTGTCCCCGCGTCCATCTTTACCGCTCTCTTGGACCTGTCACAAAGGAGTCGC 79

Qy       71 GCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGTCAGTGCCACA 130
Db       80 GCCGCTGTCGCTGTCCCCTCCCTCCGGTGGGCCCAGGAGCTAGTGCAAGTCAGTGCCACA 139

Qy      131 GCCCGACCGCGCTGCTCTGAG-----CCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGG 185
Db      140 GCCCGACCGCGCTGCTCTGGGAAGCCCCTTGGGGACGTGGCCGGGGAGGGAGCTTGAGGG 199

Qy      186 TTGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGACT 245
Db      200 CTAGCGACGCCTGTGAAGGAAGGGGACAGCCGCTGAAGCCTGGGTCGGAGAGACTGGACT 259

Qy      246 GGGGCCGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAACCTGAG 305
Db      260 GGGGCCGTGGCCGTCTCCGGGCAGGGGTCTTGGAGAGGGTGGCGTTGGTCAGAGCCTGGG 319

Qy      306 AAACAGCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCCTAGA 365
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Qy      366 AGAGGGTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCCCTTCT 425
Db      380 AAGAGGGTGTTCCCCTTTAGGGGATCTTGACTGAAGGAGGTCCT--GGGGTCACCCTCCC 437

Qy      426 GAGGAGGCTGCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCTGTAGT 485
Db      438 GAGGAGAC-----------CGGCTAAGAACTGCCAGTGTATGGCCAGCATTCCCAGTGGT 486

Qy      486 TGATAATGTTGGGAATAAGCTCTGCAACTTTCTTTGGCATTCAGTTGTTAAAAACAAATA 545
Db      487 TGATAATGTTGGAAATGAGCTGCTTGACCTTCTCCAGCATTCAGTTGTTAAAAATGAATA 546

Qy      546 GGATGCAAATTCCTCAACTCCAGGTTATGAAAACAGTACTTGGAAAACTGAAAACTACCT 605
Db      547 GAATGCAAGT---TCAGTTCCACATTATGAAAACAGTACTCGGAAAATTGAAAACTATCT 603

Qy      606 AAATGATCGTCTTTGGTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGT 665
Db      604 AGATGATTGTCTTTGGTTGGGCTGTGTTCTTAGCAAGCAGAAGCCTTGGTCAGGGTCTGC 663

Qy      666 TGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTACTACCA 725
Db      664 TGCTGACTCTTGAGGAGCACATAGCCCACCTATTGGGGACTACAGGTGCCACTGCTACTA 723

Qy      726 TGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACACCCAAC 785
Db      724 TGGGTAATTCCTGCATCTGCCGAGATGACAGTGGAGCAGAAGACAATGTTGACACCCACC 783

Qy      786 AGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACACAAGGAGCCAACCACGGGACC 845
Db      784 AGCAACAGGCTGAGAACAGTACAGTCCCTACTGCTGATAGTAGGAGCCAACCTCGGGACC 843

Qy      846 CTGTTCGGCCACCAAGGAGGGGCCGAGGACCTCATGAGCCAAGGAGAAAGAAACAAAATG 905
Db      844 CTGTCCGGCCTCCAAGGAGAGGCCGAGGACCTCATGAGCCAAGGAGAAAGAAACAAAATG 903

Qy      906 TGGATGGGCTAGTGTTGGACACACTGGCAGTAATACGGACTCTTGTAGATAA 957
Db      904 TGGATGGGTTAGTGCTGGACACACTGGCGGTAATACGGACTCTTGTAGATAA 955
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RESULT 6
CB295706
LOCUS       CB295706                 591 bp    mRNA    linear   EST 28-FEB-2003
DEFINITION  12B22056_rev_1_A02_r_005.ab1 Chimpanzee brain library Koos Pan
            troglodytes cDNA clone 12B22056_rev_1_A02_r_005.ab1 5', mRNA
            sequence.
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ACCESSION   CB295706
VERSION     CB295706.1  GI:28621136
KEYWORDS    EST.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Hellmann,I., Zollner,S., Enard,W., Ebersberger,I., Nickel,B. and
            Paabo,S.
  TITLE     Selection on human genes as revealed by comparisons to chimpanzee
            cDNA
  JOURNAL   Genome Res. (2003) In press
COMMENT     Contact: Paabo S
            Evolutionary Genetics
            Max-Planck-Institute for evolutionary Anthropology
            Deutscher Platz 6, 04103 Leipzig, Germany
            Tel: +49-(0)-341-3550 500
            Fax: +49-(0)-341-3550 555
            Email: paabo@eva.mpg.de
            Seq primer: M13 reverse.
FEATURES             Location/Qualifiers
     source          1. .591
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                     /mol_type="mRNA"
                     /db_xref="taxon:9598"
                     /clone="12B22056_rev_1_A02_r_005.ab1"
                     /sex="male"
                     /tissue_type="brain, presumably cortex"
                     /dev_stage="adult"
                     /lab_host="Epicurian Coli (TM) XL-10-Gold"
                     /clone_lib="Chimpanzee brain library Koos"
                     /note="Vector: pUChi; Site_1: SfiI-A; Site_2: SfiI-B; The
                     library was prepared using the SMART cDNA library
                     construction Kit (Clontech), doing only primer extension,
                     but not PCR amplification of the cDNA. The only deviation
                     from the published protocoll was that we cloned the cDNA
                     into a plasmid Vector."
ORIGIN

  Query Match             47.8%;  Score 582.8;  DB 14;  Length 591;
  Best Local Similarity   99.3%;  Pred. No. 1.4e-137;
  Matches  584;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        265 GAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACAGCCGAGAGGTTTTC 324
              | | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 GGANNGGCCCGGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACAGCCGAGAGGTTTTC 63

Qy        325 CACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCCTAGAAGAGGGTGTTCCCTCTTTC 384
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 CACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCCTAGAAGAGGGTGTTCCCTCTTTC 123

Qy        385 GGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCCCTTCTGAGGAGGCTGCGGCTAACA 444
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 GGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCCCTTCTGAGGAGGCTGCGGCTAACA 183

Qy        445 GGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCTGTAGTTGATAATGTTGGGAATAAG 504
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Db        184 GGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCTGTAGTTGATAATGTTGGGAATAAG 243

Qy        505 CTCTGCAACTTTCTTTGGCATTCAGTTGTTAAAAACAAATAGGATGCAAATTCCTCAACT 564
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 CTCTGCAACTTTCTTTGGCATTCAGTTGTTAAAAACAAATAGGATGCAAATTCCTCAACT 303

Qy        565 CCAGGTTATGAAAACAGTACTTGGAAAACTGAAAACTACCTAAATGATCGTCTTTGGTTG 624
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 CCAGGTTATGAAAACAGTACTTGGAAAACTGAAAACTACCTAAATGATCGTCTTTGGTTG 363

Qy        625 GGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAGCA 684
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 GGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAGCA 423

Qy        685 CATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTG 744
              ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        424 CATAGCCCACTTCCTAGGGACTGGAGGTGCTGCTACTACCATGGGTAATTCCTGTATCTG 483

Qy        745 CCGAGATGACAGTGGAACAGATGACAGTGTTGACACCCAACAGCAACAGGCCGAGAACAG 804
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 CCGAGATGACAGTGGAACAGATGACAGTGTTGACACCCAACAGCAACAGGCCGAGAACAG 543

Qy        805 TGCAGTACCCACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTCG 852
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Db        544 TGCAGTACCCACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTCG 591


RESULT 7
BU152634
LOCUS       BU152634                892 bp    mRNA    linear   EST 03-SEP-2002
DEFINITION  AGENCOURT_8750338 NIH_MGC_130 Mus musculus cDNA clone IMAGE:6333149
            5', mRNA sequence.
ACCESSION   BU152634
VERSION     BU152634.1  GI:22666166
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 892)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freeman,
            Ph.D.
             cDNA Library Preparation: ResGen, Invitrogen Corp
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13791  row: o  column: 06
            High quality sequence stop: 721.
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                     /note="Organ: otocysts; Vector: pCMV-SPORT6.1; Site_1:
                     EcoRV; Site_2: NotI; Cloned unidirectionally.  Primer:
                     Oligo dT.  Average insert size 1.95  kb.  Constructed by
                     ResGen, Invitrogen Corp. Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             45.2%;  Score 550.4;  DB 13;  Length 892;
  Best Local Similarity   79.2%;  Pred. No. 3.1e-129;
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Qy         40 CGTTCTCTCGGACCTGTCACAAAGGAGTCGCGCCGCCGCCGCCGCCCCCTCCCTCCGGTG 99
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Db          1 CGCTCTCTTGGACCTGTCACAAAGGAGTCGCGCCGCTGTCGCTGTCCCCTCCCTCCGGTG 60

Qy        100 GGCCCGGGAGGTAGAGAAAGTCAGTGCCACAGCCCGACCGCGCTGCTCTGAG-----CCC 154
              ||||| |||| ||| | |||||||||||||||||||||||||||||| |     ||
Db         61 GGCCCAGGAGCTAGTGCAAGTCAGTGCCACAGCCCGACCGCGCTGCTCTGGGAAGCCCCT 120

Qy        155 TGGGCACGCGGAACGGGAGGGAGTCTGAGGGTTGGGGACGTCTGTGAGGGAGGGGAACAG 214
              |||| ||| ||   |||||||| |||||| | | |||| |||||| ||| ||| ||||
Db        121 TGGGGACGTGGCCGGGGAGGGAGCTTGAGGGCTAGCGACGCCTGTGAAGGAAGGGGACAG 180

Qy        215 CCGCTCGAGCCTGGGGCGGGCGGACCGGACTGGGGCCGGGGTAGGCTCTGGAAAGGGCCC 274
              ||||| |||||||| ||| ||| |||||||||||| || | ||| || |||| |
Db        181 CCGCTGAAGCCTGGGTCGGAGAGACTGGACTGGGGCCGTGGCCGTCTCCGGGCAGGGGTC 240
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Qy        275 GGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACAGCCGAGAGGTTTTCCACCGAGGCC 334
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Qy        335 CGCGCTTGAGGGATCTGAAGAGGTTCCTAGAAGAGGGTGTTCCCTCTTTCGGGGGTCCTC 394
Db        301 CGCGCTGGAGGCGCCTGAAAGCGGTTCCTGGAAGAGGGTGTTCCCCTTTAGGGGATCTTG 360

Qy        395 ACCAGAAGAGGTTCTTGGGGGTCGCCCTTCTGAGGAGGCTGCGGCTAACAGGGCCCAGAA 454
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Qy        455 CTGCCATTGGATGTCCAGAATCCCCTGTAGTTGATAATGTTGGGAATAAGCTCTGCAACT 514
Db        408 CTGCCAGTGTATGGCCAGCATTCCCAGTGGTTGATAATGTTGGAAATGAGCTGCTTGACC 467

Qy        515 TTCTTTGGCATTCAGTTGTTAAAAACAAATAGGATGCAAATTCCTCAACTCCAGGTTATG 574
Db        468 TTCTCCAGCATTCAGTTGTTAAAAATGAATAGAATGCAAGT---TCAGTTCCACATTATG 524

Qy        575 AAAACAGTACTTGGAAAACTGAAAACTACCTAAATGATCGTCTTTGGTTGGGCCGTGTTC 634
Db        525 AAAACAGTACTCGGAAAATTGAAAACTATCTAGATGATTGTCTTTGGTTGGGCTGTGTTC 584

Qy        635 TTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAGCACATAGCCCAC 694
Db        585 TTAGCAAGCAGAAGCCTTGGTCAGGGTCTGCTGCTGACTCTTGAGGAGCACATAGCCCAC 644

Qy        695 TTCCTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTGCCGAGATGAC 754
Db        645 CTATTGGGGACTACAGGTGCCACTGCTACTATGGGTAATTCCTGCATCTGCCGAGATGAC 704

Qy        755 AGTGGAACAGATGACAGTGTTGACACCCAACAGCAACAGGCCGAGAACAGTGCAGTACCC 814
Db        705 AGTGGAGCAGAAGACAATGTTGACACCCACCAGCAACAGGCTGAGAACAGTACAGTCCCT 764

Qy        815 ACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTCGGCCACCAAGGAGGGGCCGAGGA 874
Db        765 ACTGCTGATAGTAGGAGCCAACCTCGGGACCCTGTCCGGCCTCCAAGGAGAGGCCGAGGA 824

Qy        875 CCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTTGGACACACTGG 932
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RESULT 8
BG744401

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LOCUS       BG744401                722 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602723139F1 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:4849713 5',
            mRNA sequence.
ACCESSION   BG744401
VERSION     BG744401.1  GI:14055054
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 722)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1689  row: m  column: 10
            High quality sequence stop: 678.
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                     /clone="IMAGE:4849713"
                     /tissue_type="natural killer cells, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_106"
                     /note="Organ: blood; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN
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  Query Match             44.0%;  Score 535.4;  DB 12;  Length 722;
  Best Local Similarity   99.5%;  Pred. No. 1.9e-125;
  Matches  558;  Conservative    0;  Mismatches    1;  Indels    2;  Gaps    2;

Qy        398 AGAAGAGGTTCTTGGGGGTCGCCCTTCTGAGGAGGCTGCGGCTAACAGGGCCCAGAACTG 457
Db          2 AGAAGAGGTTCTTGGGGGTCGCCCTTCTGAGGAGGCTGCGGCTAACAGGGCCCAGAACTG 61

Qy        458 CCATTGGATGTCCAGAATCCCCTGTAGTTGATAATGTTGGGAATAAGCTCTGCAACTTTC 517
Db         62 CCATAGGATGTCCAGAATCCCCTGTAGTTGATAATGTTGGGAATAAGCTCTGCAACTTTC 121

Qy        518 TTTGGCATTCAGTTGTTAAAAACAAATAGGATGCAAATTCCTCAACTCCAGGTTATGAAA 577
Db        122 TTTGGCATTCAGTTGTTAAAAACAAATAGGATGCAAATTCCTCAACTCCAGGTTATGAAA 181

Qy        578 ACAGTACTTGGAAAACTGAAAACTACCTAAATGATCGTCTTTGGTTGGGCCGTGTTCTTA 637
Db        182 ACAGTACTTGGAAAACTGAAAACTACCTAAATGATCGTC-TTGGTTGGGCCGTGTTCTTA 240

Qy        638 GCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTC 697
Db        241 GCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTC 300

Qy        698 CTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTGCCGAGATGACAGT 757
Db        301 CTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTGCCGAGATGACAGT 360

Qy        758 GGAACAGATGACAGTGTTGACACCCAACAGCAACAGG-CCGAGAACAGTGCAGTACCCAC 816
Db        361 GGAACAGATGACAGTGTTGACACCCAACAGCAACAGGCCCGAGAACAGTGCAGTACCCAC 420

Qy        817 TGCTGACACAAGGAGCCAACCACGGGACCCTGTTCGGCCACCAAGGAGGGGCCGAGGACC 876
Db        421 TGCTGACACAAGGAGCCAACCACGGGACCCTGTTCGGCCACCAAGGAGGGGCCGAGGACC 480

Qy        877 TCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTTGGACACACTGGCAGT 936
Db        481 TCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTTGGACACACTGGCAGT 540

Qy        937 AATACGGACTCTTGTAGATAA 957
Db        541 AATACGGACTCTTGTAGATAA 561
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RESULT 9
BI666950

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LOCUS       BI666950                711 bp    mRNA    linear   EST 12-SEP-2001
DEFINITION  603291808F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5311345 5',
            mRNA sequence.
ACCESSION   BI666950
VERSION     BI666950.1  GI:15581183
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
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  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 711)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11788  row: p  column: 02
            High quality sequence stop: 695.
FEATURES             Location/Qualifiers
     source          1. .711
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5311345"
                     /tissue_type="hypothalamus"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_96"
                     /note="Organ: brain; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
                     (gtcgag); Oligo-dT primed using primer
                     5'-TTTTTTTTTTTTTTTVN-3', size-selected for average
                     insert size 2.3 kb and normalized to ROT 5. This is a
                     primary library enriched for full-length clones and
                     constructed using the Cap-trapper method (Carninci, in
                     preparation). Library constructed by M. Brownstein
                     (NIMH/NHGRI, National Institutes of Health). Note: this is
                     a NIH_MGC Library."
ORIGIN

  Query Match            41.5%;  Score 505.4;  DB 12;  Length 711;
  Best Local Similarity  99.8%;  Pred. No. 8.7e-118;
  Matches  506;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        451 AGAACTGCCATTGGATGTCCAGAATCCCCTGTAGTTGATAATGTTGGGAATAAGCTCTGC 510
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Db        142 AAAACTGCCATTGGATGTCCAGAATCCCCTGTAGTTGATAATGTTGGGAATAAGCTCTGC 201

Qy        511 AACTTTCTTTGGCATTCAGTTGTTAAAAACAAATAGGATGCAAATTCCTCAACTCCAGGT 570
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 AACTTTCTTTGGCATTCAGTTGTTAAAAACAAATAGGATGCAAATTCCTCAACTCCAGGT 261

Qy        571 TATGAAAACAGTACTTGGAAAACTGAAAACTACCTAAATGATCGTCTTTGGTTGGGCCGT 630
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Db        262 TATGAAAACAGTACTTGGAAAACTGAAAACTACCTAAATGATCGTCTTTGGTTGGGCCGT 321

Qy        631 GTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAGCACATAGC 690
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        322 GTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAGCACATAGC 381

Qy        691 CCACTTCCTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTGCCGAGA 750
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Db        382 CCACTTCCTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTGCCGAGA 441

Qy        751 TGACAGTGGAACAGATGACAGTGTTGACACCCAACAGCAACAGGCCGAGAACAGTGCAGT 810
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Db        442 TGACAGTGGAACAGATGACAGTGTTGACACCCAACAGCAACAGGCCGAGAACAGTGCAGT 501

Qy        811 ACCCACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTCGGCCACCAAGGAGGGGCCG 870
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Db        502 ACCCACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTCGGCCACCAAGGAGGGGCCG 561

Qy        871 AGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTTGGACACACT 930
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Db        562 AGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTTGGACACACT 621

Qy        931 GGCAGTAATACGGACTCTTGTAGATAA 957
              |||||||||||||||||||||||||||
Db        622 GGCAGTAATACGGACTCTTGTAGATAA 648


RESULT 10
BU161287
LOCUS       BU161287                 835 bp    mRNA    linear   EST 04-SEP-2002
DEFINITION  AGENCOURT_7960449 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6166363
            5', mRNA sequence.
ACCESSION   BU161287
VERSION     BU161287.1  GI:22675197
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 835)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13526  row: i  column: 20
            High quality sequence stop: 634.
FEATURES             Location/Qualifiers
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                     /clone="IMAGE:6166363"
                     /tissue_type="melanotic melanoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_72"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 2 kb.  Library constructed by Life
                     Technologies."
ORIGIN

  Query Match            41.5%;  Score 505.4;  DB 13;  Length 835;
  Best Local Similarity  99.8%;  Pred. No. 9.2e-118;
  Matches  506;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        451 AGAACTGCCATTGGATGTCCAGAATCCCCTGTAGTTGATAATGTTGGGAATAAGCTCTGC 510
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Qy        511 AACTTTCTTTGGCATTCAGTTGTTAAAAACAAATAGGATGCAAATTCCTCAACTCCAGGT 570
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Db        125 AACTTTCTTTGGCATTCAGTTGTTAAAAACAAATAGGATGCAAATTCCTCAACTCCAGGT 184

Qy        571 TATGAAAACAGTACTTGGAAAACTGAAAACTACCTAAATGATCGTCTTTGGTTGGGCCGT 630
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Db        185 TATGAAAACAGTACTTGGAAAACTGAAAACTACCTAAATGATCGTCTTTGGTTGGGCCGT 244

Qy        631 GTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAGCACATAGC 690
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Db        245 GTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAGCACATAGC 304

Qy        691 CCACTTCCTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTGCCGAGA 750
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Db        305 CCACTTCCTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTGCCGAGA 364
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Qy        751 TGACAGTGGAACAGATGACAGTGTTGACACCCAACAGCAACAGGCCGAGAACAGTGCAGT 810
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Db        365 TGACAGTGGAACAGATGACAGTGTTGACACCCAACAGCAACAGGCCGAGAACAGTGCAGT 424

Qy        811 ACCCACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTCGGCCACCAAGGAGGGGCCG 870
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Db        425 ACCCACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTCGGCCACCAAGGAGGGGCCG 484

Qy        871 AGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTTGGACACACT 930
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        485 AGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTTGGACACACT 544

Qy        931 GGCAGTAATACGGACTCTTGTAGATAA 957
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Db        545 GGCAGTAATACGGACTCTTGTAGATAA 571
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RESULT 11
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LOCUS       BU500574                857 bp    mRNA    linear   EST 12-SEP-2002
DEFINITION  AGENCOURT_7859738 NIH_MGC_64 Homo sapiens cDNA clone IMAGE:6108995
            5', mRNA sequence.
ACCESSION   BU500574
VERSION     BU500574.1  GI:22801691
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 857)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: NIMH/LOG
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2354  row: c  column: 12
            High quality sequence stop: 653.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:6108995"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_64"
                     /note="Vector: pOTB7a; Site_1: CeuI; Site_2: SceI; This
                     library is a size selection of NIH_MGC_35, from 3.0-4.5
                     kb. Size selection done at the National Institute of
                     Mental Health, NIH. Note: this is a NIH_MGC Library."
ORIGIN

  Query Match           41.5%;  Score 505.4;  DB 13;  Length 857;
  Best Local Similarity   99.8%;  Pred. No. 9.3e-118;
  Matches  506;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        451 AGAACTGCCATTGGATGTCCAGAATCCCCTGTAGTTGATAATGTTGGGAATAAGCTCTGC 510
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 AAAACTGCCATTGGATGTCCAGAATCCCCTGTAGTTGATAATGTTGGGAATAAGCTCTGC 165

Qy        511 AACTTTCTTTGGCATTCAGTTGTTAAAAACAAATAGGATGCAAATTCCTCAACTCCAGGT 570
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 AACTTTCTTTGGCATTCAGTTGTTAAAAACAAATAGGATGCAAATTCCTCAACTCCAGGT 225

Qy        571 TATGAAAACAGTACTTGGAAAACTGAAAACTACCTAAATGATCGTCTTTGGTTGGGCCGT 630
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Db        226 TATGAAAACAGTACTTGGAAAACTGAAAACTACCTAAATGATCGTCTTTGGTTGGGCCGT 285

Qy        631 GTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAGCACATAGC 690
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 GTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAGCACATAGC 345

Qy        691 CCACTTCCTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTGCCGAGA 750
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Db        346 CCACTTCCTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTGCCGAGA 405

Qy        751 TGACAGTGGAACAGATGACAGTGTTGACACCCAACAGCAACAGGCCGAGAACAGTGCAGT 810
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Db        406 TGACAGTGGAACAGATGACAGTGTTGACACCCAACAGCAACAGGCCGAGAACAGTGCAGT 465

Qy        811 ACCCACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTCGGCCACCAAGGAGGGGCCG 870
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Db        466 ACCCACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTCGGCCACCAAGGAGGGGCCG 525

Qy        871 AGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTTGGACACACT 930
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Qy        931 GGCAGTAATACGGACTCTTGTAGATAA 957
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Db        586 GGCAGTAATACGGACTCTTGTAGATAA 612
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RESULT 12
BQ439291
LOCUS       BQ439291                871 bp    mRNA    linear   EST 24-MAY-2002
DEFINITION  AGENCOURT_7764766 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:6013976
            5', mRNA sequence.
ACCESSION   BQ439291
VERSION     BQ439291.1  GI:21178367
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 871)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13207  row: l  column: 09
            High quality sequence stop: 653.
FEATURES             Location/Qualifiers
     source          1. .871
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6013976"
                     /tissue_type="embryonal carcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_92"
                     /note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 2.5 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match           41.5%;  Score 505.4;  DB 13;  Length 871;
  Best Local Similarity   99.8%;  Pred. No. 9.4e-118;
  Matches  506;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy        451 AGAACTGCCATTGGATGTCCAGAATCCCCTGTAGTTGATAATGTTGGGAATAAGCTCTGC 510
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Db        107 AAAACTGCCATTGGATGTCCAGAATCCCCTGTAGTTGATAATGTTGGGAATAAGCTCTGC 166

Qy        511 AACTTTCTTTGGCATTCAGTTGTTAAAAACAAATAGGATGCAAATTCCTCAACTCCAGGT 570
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        167 AACTTTCTTTGGCATTCAGTTGTTAAAAACAAATAGGATGCAAATTCCTCAACTCCAGGT 226

Qy        571 TATGAAAACAGTACTTGGAAAACTGAAAACTACCTAAATGATCGTCTTTGGTTGGGCCGT 630
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Db        227 TATGAAAACAGTACTTGGAAAACTGAAAACTACCTAAATGATCGTCTTTGGTTGGGCCGT 286

Qy        631 GTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAGCACATAGC 690
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Db        287 GTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAGCACATAGC 346

Qy        691 CCACTTCCTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTGCCGAGA 750
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Db        347 CCACTTCCTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTGCCGAGA 406

Qy        751 TGACAGTGGAACAGATGACAGTGTTGACACCCAACAGCAACAGGCCGAGAACAGTGCAGT 810
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        407 TGACAGTGGAACAGATGACAGTGTTGACACCCAACAGCAACAGGCCGAGAACAGTGCAGT 466

Qy        811 ACCCACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTCGGCCACCAAGGAGGGGCCG 870
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        467 ACCCACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTCGGCCACCAAGGAGGGGCCG 526

Qy        871 AGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTTGGACACACT 930
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        527 AGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTTGGACACACT 586

Qy        931 GGCAGTAATACGGACTCTTGTAGATAA 957
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Db        587 GGCAGTAATACGGACTCTTGTAGATAA 613
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RESULT 13
CD683922
LOCUS CD683922 670 bp mRNA linear EST 25-JUN-2003
DEFINITION EST442 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION CD683922
VERSION CD683922.1 GI:32198428
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 670)
AUTHORS Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
Zeng,Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: YiXin Zeng
Cancer Center
Sun Yat-sen University
651 DongFeng Road East, GuangZhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn.
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA
library from southern Chinese"
ORIGIN

Query Match 41.4%; Score 503.8; DB 14; Length 670;

Best Local Similarity 99.6%; Pred. No. 2.2e-117;
Matches 505; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy        451 AGAACTGCCATTGGATGTCCAGAATCCCCTGTAGTTGATAATGTTGGGAATAAGCTCTGC 510
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Db        146 AAAACTGCCATTGGATGTCCAGAATCCCCTGTAGTTGATAATGTTGGGAATAAGCTCTGC 205

Qy        511 AACTTTCTTTGGCATTCAGTTGTTAAAAACAAATAGGATGCAAATTCCTCAACTCCAGGT 570
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Qy        571 TATGAAAACAGTACTTGGAAAACTGAAAACTACCTAAATGATCGTCTTTGGTTGGGCCGT 630
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Db        266 TATGAAAACAGTACTTGGAAAACTGAAAACTACCTAAATGATCGTCTTTGGTTGGGCCGT 325

Qy        631 GTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAGCACATAGC 690
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        326 GTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAGCACATAGC 385

Qy        691 CCACTTCCTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTGCCGAGA 750
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Db        386 CCACTTCCTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTGCCGAGA 445

Qy        751 TGACAGTGGAACAGATGACAGTGTTGACACCCAACAGCAACAGGCCGAGAACAGTGCAGT 810
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Db        446 TGACAGTGGAACAGATGACAGTGTTGACACCCAACAGCAACAGGCCGAGAACAGTGCAGT 505

Qy        811 ACCCACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTCGGCCACCAAGGAGGGGCCG 870
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Db        506 ACCCACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTCGGCCACCAAGGAGGGGCCG 565

Qy        871 AGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTTGGACACACT 930
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Db        566 AGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTTGGACACACT 625

Qy        931 GGCAGTAATACGGACTCTTGTAGATAA 957
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Db        626 GGCAGTAATACGGACTCTTGTAGATCA 652
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RESULT 14
BG749354
LOCUS BG749354 727 bp mRNA linear EST 15-MAY-2001
DEFINITION 602707829F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4844622 5',
mRNA sequence.
ACCESSION BG749354
VERSION BG749354.1 GI:14060007
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 727)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1682 row: i column: 07
High quality sequence stop: 723.
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/clone="IMAGE:4844622"

/tissue_type="normal pigmented retinal epithelium"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_43"
/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library. |"

ORIGIN

Query Match 41.4%; Score 503.8; DB 12; Length 727;
Best Local Similarity 99.6%; Pred. No. 2.2e-117;
Matches 505; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      511 AACTTTCTTTGGCATTCAGTTGTTAAAAACAAATAGGATGCAAATTCCTCAACTCCAGGT 570
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Db      213 AACTTTCTTTGGCATTCAGTTGTTAAAAACAAATAGGATGCAAATTCCTCAACTCCAGGT 272

Qy      571 TATGAAAACAGTACTTGGAAAACTGAAAACTACCTAAATGATCGTCTTTGGTTGGGCCGT 630
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Db      273 TATGAAAACAGTACTTGGAAAACTGAAAACTACCTAAATGATCGTCTTTGGTTGGGCCGT 332

Qy      631 GTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAGCACATAGC 690
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Db      333 GTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAGCACATAGC 392

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RESULT 15
BI668768
LOCUS BI668768 834 bp mRNA linear EST 12-SEP-2001
DEFINITION 603294714F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5313938 5', mRNA sequence.
ACCESSION BI668768
VERSION BI668768.1 GI:15583001
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 834)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11795 row: 1 column: 03
High quality sequence stop: 810.
FEATURES Location/Qualifiers
source 1. .834
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone_lib="NIH_MGC_96"
/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 41.4%; Score 503.8; DB 12; Length 834;
Best Local Similarity 99.6%; Pred. No. 2.4e-117;
Matches 505; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      451 AGAACTGCCATTGGATGTCCAGAATCCCCTGTAGTTGATAATGTTGGGAATAAGCTCTGC 510
            | ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db      142 AAAACTGCCATTGGATGTCCAGAATCCCCTGTAGTTGATAATGTTGGGAATAAGCTCTGC 201

Qy      511 AACTTTCTTTGGCATTCAGTTGTTAAAAACAAATAGGATGCAAATTCCTCAACTCCAGGT 570
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Db      202 AACTTTCTTTGGCATTCAGTTGTTAAAAACAAATAGGATGCAAATTCCTCAACTCCAGGT 261

Qy      571 TATGAAAACAGTACTTGGAAAACTGAAAACTACCTAAATGATCGTCTTTGGTTGGGCCGT 630
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Db      262 TATGAAAACAGTACTTGGAAAACTGAAAACTACCTAAATGATCGTCTTTGGTTGGGCCGT 321

Qy      631 GTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAGCACATAGC 690
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Db      322 GTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAGCACATAGC 381

Qy      691 CCACTTCCTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTGCCGAGA 750
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      382 CCACTTCCTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTGCCGAGA 441

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Search completed: April 4, 2004, 09:00:42
Job time : 3085 secs

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XX
PA (GETH) GENENTECH INC.
XX
PI Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
XX
DR WPI; 2000-237871/20.
DR P-PSDB; AAY99341.
XX
PT New mammalian DNA sequences encoding transmembrane, receptor or secreted
PT PRO polypeptides, useful for screening of potential peptide or small
PT molecule inhibitors of the relevant receptor/ligand interactions.
XX
PS Claim 2; Fig 3; 773pp; English.
XX
CC AAA37022 to AAA37144 encode the new isolated human transmembrane,
CC receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The
CC transmembrane and receptor PRO proteins can be used for screening of
CC potential peptide or small molecule inhibitors of the relevant
CC receptor/ligand interactions. The polypeptides and nucleotide sequences
CC encoding then have various industrial applications, including uses as
CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR
CC primers and hybridisation probes used in the isolation of the PRO
CC polypeptides from the present invention
XX
SQ Sequence 1218 BP; 292 A; 299 C; 360 G; 267 T; 0 U; 0 Other;

Query Match 100.0%; Score 1218; DB 3; Length 1218;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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DT 02-APR-2001 (first entry)
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KW Secreted; transmembrane; gene therapy; ss.
XX
OS Unidentified.
XX
PN WO200078961-A1.
XX
PD 28-DEC-2000.
XX
PF 18-FEB-2000; 2000WO-US004342.
XX
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 29-OCT-1999; 99US-0162506P.
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PR 02-DEC-1999; 99WO-US028551.
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PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX
DR WPI; 2001-071395/08.
XX
PT Secreted and transmembrane proteins and nucleic acids designated PRO,
PT useful as hybridization probes, in chromosome and gene mapping and gene
PT therapy.
XX
PS Claim 2; Fig 3; 787pp; English.
XX
CC The present invention relates to secreted and transmembrane proteins.
CC These proteins and the DNA encoding them may be used as hybridization
CC probes, in chromosome and gene mapping and in the generation of anti-
CC sense RNA and DNA. They may also be used used to generate either
CC transgenic animals or knockout animals which are in turn useful for
CC development and screening of therapeutically useful reagents. The nucleic
CC acids may also be used in gene therapy
XX
SQ Sequence 1218 BP; 292 A; 299 C; 360 G; 267 T; 0 U; 0 Other;

Query Match 100.0%; Score 1218; DB 4; Length 1218;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        301 CTGAGAAACAGCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTC 360
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Db        301 CTGAGAAACAGCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTC 360

Qy        361 CTAGAAGAGGGTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTAGAAGAGGGTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCC 420

Qy        421 CTTCTGAGGAGGCTGCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTTCTGAGGAGGCTGCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCT 480

Qy        481 GTAGTTGATAATGTTGGGAATAAGCTCTGCAACTTTCTTTGGCATTCAGTTGTTAAAAAC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTAGTTGATAATGTTGGGAATAAGCTCTGCAACTTTCTTTGGCATTCAGTTGTTAAAAAC 540

Qy        541 AAATAGGATGCAAATTCCTCAACTCCAGGTTATGAAAACAGTACTTGGAAAACTGAAAAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AAATAGGATGCAAATTCCTCAACTCCAGGTTATGAAAACAGTACTTGGAAAACTGAAAAC 600

Qy        601 TACCTAAATGATCGTCTTTGGTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TACCTAAATGATCGTCTTTGGTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGG 660

Qy        661 TCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTAC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTAC 720

Qy        721 TACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACAC 780

Qy        781 CCAACAGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACACAAGGAGCCAACCACG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CCAACAGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACACAAGGAGCCAACCACG 840

Qy        841 GGACCCTGTTCGGCCACCAAGGAGGGGCCGAGGACCTCATGAGCCAAGGAGAAAGAAACA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGACCCTGTTCGGCCACCAAGGAGGGGCCGAGGACCTCATGAGCCAAGGAGAAAGAAACA 900

Qy        901 AAATGTGGATGGGCTAGTGTTGGACACACTGGCAGTAATACGGACTCTTGTAGATAAGTA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AAATGTGGATGGGCTAGTGTTGGACACACTGGCAGTAATACGGACTCTTGTAGATAAGTA 960

Qy        961 AGTATCTGACTCACGGTCACCTCCAGTGGAATGAAAAGTGTTCTGCCCGGAACCATGACT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGTATCTGACTCACGGTCACCTCCAGTGGAATGAAAAGTGTTCTGCCCGGAACCATGACT 1020

Qy       1021 TTAGGACTCCTTCAGTTCCTTTAGGACATACTCGCCAAGCCTTGTGCTCACAGGGCAAAG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTAGGACTCCTTCAGTTCCTTTAGGACATACTCGCCAAGCCTTGTGCTCACAGGGCAAAG 1080

Qy       1081 GAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAATGATAAGATTTGATGTTTTTGCTT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAATGATAAGATTTGATGTTTTTGCTT 1140

Qy       1141 GCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTCTGTAGCAGAAAACACGATAAAG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTCTGTAGCAGAAAACACGATAAAG 1200

Qy       1201 CTATGATCTTTATTAGAG 1218
              ||||||||||||||||||
Db       1201 CTATGATCTTTATTAGAG 1218
```

```
RESULT 3
AAC86965
ID   AAC86965 standard; cDNA; 1218 BP.
XX
AC   AAC86965;
XX
DT   20-APR-2001  (first entry)
XX
DE   Nucleotide sequence of human polypeptide PRO444.
XX
KW   Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO183;
KW   PRO185; PRO210; PRO215; PRO217; PRO242; PRO288; PRO365; PRO1361; PRO1308;
KW   PRO1183; PRO1272; PRO1419; PRO4999; PRO7170; PRO248; PRO353; PRO1318;
KW   PRO1600; PRO9940; PRO533; PRO301; PRO187; PRO337; PRO1411; PRO4356;
KW   PRO246; PRO265; PRO941; PRO10096; PRO6003; PRO6004; PRO350; PRO2630;
KW   PRO6309; cell death; genetic disorder; transgenic animal; gene therapy;
KW   ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             608. .961
FT                   /*tag= a
FT   sig_peptide     608. .655
FT                   /*tag= b
XX
PN   WO200077037-A2.
XX
PD   21-DEC-2000.
XX
PF   22-MAY-2000; 2000WO-US014042.
XX
PR   15-JUN-1999;   99US-0139695P.
PR   20-JUL-1999;   99US-0145070P.
PR   26-JUL-1999;   99US-0145698P.
PR   17-AUG-1999;   99US-0149396P.
PR   01-SEP-1999;   99WO-US020111.
PR   08-SEP-1999;   99WO-US020594.
PR   15-SEP-1999;   99WO-US021090.
PR   15-SEP-1999;   99WO-US021547.
PR   30-NOV-1999;   99WO-US028313.
PR   01-DEC-1999;   99WO-US028301.
PR   02-DEC-1999;   99WO-US028565.
PR   07-DEC-1999;   99US-0169495P.
PR   05-JAN-2000; 2000WO-US000219.
PR   18-FEB-2000; 2000WO-US004341.
PR   18-FEB-2000; 2000WO-US004342.
PR   22-FEB-2000; 2000WO-US004414.
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005841.
PR   20-MAR-2000; 2000WO-US007377.
PR   30-MAR-2000; 2000WO-US008439.
PR   15-MAY-2000; 2000WO-US013358.
PR   17-MAY-2000; 2000WO-US013705.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Botstein DA,  Desnoyers L,  Eaton DL;
PI   Ferrara N,  Fong S,  Gao W,  Gerber H,  Gerritsen ME,  Goddard A;
PI   Godowski PJ,  Gurney AL,  Kljavin IJ,  Mather JP,  Napier MA,  Pan J;
PI   Paoni NF,  Roy MA,  Stewart TA,  Tumas D,  Watanabe CK,  Williams PM;
PI   Wood WI,  Zhang Z;
XX
DR   WPI; 2001-050091/06.
DR   P-PSDB; AAB31180.
XX
PT   Isolated nucleic acid molecule encoding a PRO polypeptide which is a
PT   transmembrane polypeptide is useful for gene therapy and identification
PT   of related polypeptides.
XX
PS   Claim 2; Fig 3; 244pp; English.
XX
CC   The present sequence encodes a human secreted and transmembrane
CC   polypeptide. The specification describes human polypeptides, designated
CC   PRO196, PRO444, PRO183, PRO185, PRO210, PRO215, PRO217, PRO242, PRO288,
CC   PRO365, PRO1361, PRO1308, PRO1183, PRO1272, PRO1419, PRO4999, PRO7170,
CC   PRO248, PRO353, PRO1318, PRO1600, PRO9940, PRO533, PRO301, PRO187,
CC   PRO337, PRO1411, PRO4356, PRO246, PRO265, PRO941, PRO10096, PRO6003,
CC   PRO6004, PRO350, PRO2630 and PRO6309. The biological activity of cells
CC   can be modulated with agents that bind to these polypeptides, resulting
CC   in the death of the cells. The polynucleotides encoding these
```

CC polypeptides are useful in the recombinant production of the
CC polypeptides, as a hybridisation probe to screen libraries to isolate
CC homologous sequences, or to map the gene. They may also be used for
CC analysing genetic disorders, and to produce transgenic animals which are
CC useful for the development and screening of therapeutically useful
CC reagents. The polynucleotides can also be used in gene therapy e.g. to
CC replace a defective gene
XX
SQ Sequence 1218 BP; 292 A; 299 C; 360 G; 267 T; 0 U; 0 Other;

Query Match 100.0%; Score 1218; DB 4; Length 1218;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACA 60

Qy         61 AAGGAGTCGCGCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGGAGTCGCGCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGT 120

Qy        121 CAGTGCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CAGTGCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCT 180

Qy        181 GAGGGTTGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGGTTGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACC 240

Qy        241 GGACTGGGGCCGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAAC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGACTGGGGCCGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAAC 300

Qy        301 CTGAGAAACAGCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTGAGAAACAGCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTC 360

Qy        361 CTAGAAGAGGGTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTAGAAGAGGGTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCC 420

Qy        421 CTTCTGAGGAGGCTGCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTTCTGAGGAGGCTGCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCT 480

Qy        481 GTAGTTGATAATGTTGGGAATAAGCTCTGCAACTTTCTTTGGCATTCAGTTGTTAAAAAC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTAGTTGATAATGTTGGGAATAAGCTCTGCAACTTTCTTTGGCATTCAGTTGTTAAAAAC 540

Qy        541 AAATAGGATGCAAATTCCTCAACTCCAGGTTATGAAAACAGTACTTGGAAAACTGAAAAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AAATAGGATGCAAATTCCTCAACTCCAGGTTATGAAAACAGTACTTGGAAAACTGAAAAC 600

Qy        601 TACCTAAATGATCGTCTTTGGTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TACCTAAATGATCGTCTTTGGTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGG 660

Qy        661 TCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTAC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTAC 720

Qy        721 TACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACAC 780

Qy        781 CCAACAGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACACAAGGAGCCAACCACG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CCAACAGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACACAAGGAGCCAACCACG 840

Qy        841 GGACCCTGTTCGGCCACCAAGGAGGGGCCGAGGACCTCATGAGCCAAGGAGAAAGAAACA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGACCCTGTTCGGCCACCAAGGAGGGGCCGAGGACCTCATGAGCCAAGGAGAAAGAAACA 900

Qy        901 AAATGTGGATGGGCTAGTGTTGGACACACTGGCAGTAATACGGACTCTTGTAGATAAGTA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AAATGTGGATGGGCTAGTGTTGGACACACTGGCAGTAATACGGACTCTTGTAGATAAGTA 960

Qy        961 AGTATCTGACTCACGGTCACCTCCAGTGGAATGAAAAGTGTTCTGCCCGGAACCATGACT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGTATCTGACTCACGGTCACCTCCAGTGGAATGAAAAGTGTTCTGCCCGGAACCATGACT 1020

Qy       1021 TTAGGACTCCTTCAGTTCCTTTAGGACATACTCGCCAAGCCTTGTGCTCACAGGGCAAAG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTAGGACTCCTTCAGTTCCTTTAGGACATACTCGCCAAGCCTTGTGCTCACAGGGCAAAG 1080

Qy       1081 GAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAATGATAAGATTTGATGTTTTTGCTT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAATGATAAGATTTGATGTTTTTGCTT 1140

Qy       1141 GCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTCTGTAGCAGAAAACACGATAAAG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTCTGTAGCAGAAAACACGATAAAG 1200

Qy       1201 CTATGATCTTTATTAGAG 1218
              ||||||||||||||||||
Db       1201 CTATGATCTTTATTAGAG 1218
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RESULT 4
ABL88074
ID ABL88074 standard; cDNA; 1218 BP.
XX
AC ABL88074;
XX
DT 16-MAY-2002 (first entry)
XX
DE Human PRO444 cDNA sequence SEQ ID NO:5.
XX
KW Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;
KW vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
KW age-related macular degeneration; arterial restenosis; angina;
KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
KW wound healing; chromosome mapping; gene mapping; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200200690-A2.
XX
PD 03-JAN-2002.
XX
PF 20-JUN-2001; 2001WO-US019692.
XX
PR 23-JUN-2000; 2000US-0213637P.
PR 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220664P.
PR 28-JUL-2000; 2000WO-US020710.
PR 02-AUG-2000; 2000US-0222695P.
PR 17-AUG-2000; 2000US-00643657.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 24-OCT-2000; 2000US-0242922P.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 22-JAN-2001; 2001US-00767609.

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PR   28-FEB-2001; 2001US-00796498.
PR   28-FEB-2001; 2001WO-US006520.
PR   01-MAR-2001; 2001WO-US006666.
PR   09-MAR-2001; 2001US-00802706.
PR   14-MAR-2001; 2001US-00808689.
PR   22-MAR-2001; 2001US-00816744.
PR   05-APR-2001; 2001US-00828366.
PR   10-MAY-2001; 2001US-00854208.
PR   10-MAY-2001; 2001US-00854280.
PR   25-MAY-2001; 2001US-00866028.
PR   25-MAY-2001; 2001US-00866034.
PR   25-MAY-2001; 2001WO-US017092.
PR   30-MAY-2001; 2001US-00870574.
PR   30-MAY-2001; 2001WO-US017443.
PR   01-JUN-2001; 2001WO-US017800.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Ferrara N,  Gerber H,  Gerritsen ME,  Goddard A;
PI   Godowski PJ,  Gurney AL,  Hillan KJ,  Marsters SA,  Pan J,  Paoni NF;
PI   Stephan JF,  Watanabe CK,  Williams PM,  Wood WI,  Ye W;
XX
DR   WPI; 2002-090516/12.
DR   P-PSDB; ABB84819.
XX
PT   One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT   useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT   infarction), endothelial or angiogenic disorders in a mammal.
XX
PS   Claim 2; Fig 5; 565pp; English.
XX
CC   ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
CC   ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
CC   antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
CC   activities, and can be used in gene therapy. The PRO polynucleotides,
CC   proteins, agonists and antagonists are useful for treating or diagnosing
CC   a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
CC   cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
CC   atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC   angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC   angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC   healing. The PRO polynucleotides have applications in molecular biology,
CC   including use as hybridisation probes, and in chromosome and gene
CC   mapping. ABL88259 to ABL88267 represent primers and probes used in the
CC   exemplification of the present invention
XX
SQ   Sequence 1218 BP; 292 A; 299 C; 360 G; 267 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 1218;  DB 6;  Length 1218;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1218;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACA 60

Qy         61 AAGGAGTCGCGCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGGAGTCGCGCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGT 120

Qy        121 CAGTGCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CAGTGCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCT 180

Qy        181 GAGGGTTGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGGTTGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACC 240

Qy        241 GGACTGGGGCCGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAAC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGACTGGGGCCGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAAC 300

Qy        301 CTGAGAAACAGCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTGAGAAACAGCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTC 360

Qy        361 CTAGAAGAGGGTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTAGAAGAGGGTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCC 420

Qy        421 CTTCTGAGGAGGCTGCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTTCTGAGGAGGCTGCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCT 480

Qy        481 GTAGTTGATAATGTTGGGAATAAGCTCTGCAACTTTCTTTGGCATTCAGTTGTTAAAAAC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTAGTTGATAATGTTGGGAATAAGCTCTGCAACTTTCTTTGGCATTCAGTTGTTAAAAAC 540

Qy        541 AAATAGGATGCAAATTCCTCAACTCCAGGTTATGAAAACAGTACTTGGAAAACTGAAAAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AAATAGGATGCAAATTCCTCAACTCCAGGTTATGAAAACAGTACTTGGAAAACTGAAAAC 600

Qy        601 TACCTAAATGATCGTCTTTGGTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TACCTAAATGATCGTCTTTGGTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGG 660

Qy        661 TCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTAC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTAC 720

Qy        721 TACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACAC 780

Qy        781 CCAACAGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACACAAGGAGCCAACCACG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CCAACAGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACACAAGGAGCCAACCACG 840

Qy        841 GGACCCTGTTCGGCCACCAAGGAGGGGCCGAGGACCTCATGAGCCAAGGAGAAAGAAACA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGACCCTGTTCGGCCACCAAGGAGGGGCCGAGGACCTCATGAGCCAAGGAGAAAGAAACA 900

Qy        901 AAATGTGGATGGGCTAGTGTTGGACACACTGGCAGTAATACGGACTCTTGTAGATAAGTA 960
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Db        901 AAATGTGGATGGGCTAGTGTTGGACACACTGGCAGTAATACGGACTCTTGTAGATAAGTA 960

Qy        961 AGTATCTGACTCACGGTCACCTCCAGTGGAATGAAAAGTGTTCTGCCCGGAACCATGACT 1020
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Db        961 AGTATCTGACTCACGGTCACCTCCAGTGGAATGAAAAGTGTTCTGCCCGGAACCATGACT 1020

Qy       1021 TTAGGACTCCTTCAGTTCCTTTAGGACATACTCGCCAAGCCTTGTGCTCACAGGGCAAAG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTAGGACTCCTTCAGTTCCTTTAGGACATACTCGCCAAGCCTTGTGCTCACAGGGCAAAG 1080

Qy       1081 GAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAATGATAAGATTTGATGTTTTTGCTT 1140
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Db       1081 GAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAATGATAAGATTTGATGTTTTTGCTT 1140

Qy       1141 GCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTCTGTAGCAGAAAACACGATAAAG 1200
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Db       1141 GCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTCTGTAGCAGAAAACACGATAAAG 1200

Qy       1201 CTATGATCTTTATTAGAG 1218
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Db       1201 CTATGATCTTTATTAGAG 1218


RESULT 5
ABL95563
ID   ABL95563 standard; cDNA; 1218 BP.
XX
AC   ABL95563;
XX
DT   19-JUL-2002  (first entry)
XX
DE   Human angiogenesis related cDNA PRO444 SEQ ID NO: 5.
```

XX
KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;
KW antiarteriosclerotic; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200208284-A2.
XX
PD 31-JAN-2002.
XX
PF 09-JUL-2001; 2001WO-US021735.
XX
PR 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220664P.
PR 28-JUL-2000; 2000WO-US020710.
PR 02-AUG-2000; 2000US-0222695P.
PR 17-AUG-2000; 2000US-00643657.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 24-OCT-2000; 2000US-0242922P.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 22-JAN-2001; 2001US-00767609.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
XX
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
DR WPI; 2002-171999/22.
DR P-PSDB; ABB95425.

XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.
XX
PS Claim 1; Fig 5; 567pp; English.
XX
CC The present invention provides the protein and coding sequences of human
CC PRO proteins. These are useful for treating or diagnosing a
CC cardiovascular, endothelial or angiogenic disorder, including cardiac
CC hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The present sequence is a coding sequence of the invention
XX
SQ Sequence 1218 BP; 292 A; 299 C; 360 G; 267 T; 0 U; 0 Other;

Query Match 100.0%; Score 1218; DB 6; Length 1218;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACA 60
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Db          1 CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACA 60

Qy         61 AAGGAGTCGCGCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGT 120
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Db         61 AAGGAGTCGCGCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGT 120

Qy        121 CAGTGCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCT 180
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Db        121 CAGTGCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCT 180

Qy        181 GAGGGTTGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACC 240
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Qy        241 GGACTGGGGCCGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAAC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGACTGGGGCCGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAAC 300

Qy        301 CTGAGAAACAGCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTC 360
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Db        301 CTGAGAAACAGCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTC 360

Qy        361 CTAGAAGAGGGTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCC 420
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Db        361 CTAGAAGAGGGTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCC 420

Qy        421 CTTCTGAGGAGGCTGCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCT 480
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Db        421 CTTCTGAGGAGGCTGCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCT 480

Qy        481 GTAGTTGATAATGTTGGGAATAAGCTCTGCAACTTTCTTTGGCATTCAGTTGTTAAAAAC 540
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Db        481 GTAGTTGATAATGTTGGGAATAAGCTCTGCAACTTTCTTTGGCATTCAGTTGTTAAAAAC 540

Qy        541 AAATAGGATGCAAATTCCTCAACTCCAGGTTATGAAAACAGTACTTGGAAAACTGAAAAC 600
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Db        541 AAATAGGATGCAAATTCCTCAACTCCAGGTTATGAAAACAGTACTTGGAAAACTGAAAAC 600

Qy        601 TACCTAAATGATCGTCTTTGGTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TACCTAAATGATCGTCTTTGGTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGG 660

Qy        661 TCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTAC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTAC 720

Qy        721 TACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACAC 780
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Db        721 TACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACAC 780
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Qy        781 CCAACAGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACACAAGGAGCCAACCACG 840
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Db        781 CCAACAGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACACAAGGAGCCAACCACG 840

Qy        841 GGACCCTGTTCGGCCACCAAGGAGGGGCCGAGGACCTCATGAGCCAAGGAGAAAGAAACA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        901 AAATGTGGATGGGCTAGTGTTGGACACACTGGCAGTAATACGGACTCTTGTAGATAAGTA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AAATGTGGATGGGCTAGTGTTGGACACACTGGCAGTAATACGGACTCTTGTAGATAAGTA 960

Qy        961 AGTATCTGACTCACGGTCACCTCCAGTGGAATGAAAAGTGTTCTGCCCGGAACCATGACT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGTATCTGACTCACGGTCACCTCCAGTGGAATGAAAAGTGTTCTGCCCGGAACCATGACT 1020

Qy       1021 TTAGGACTCCTTCAGTTCCTTTAGGACATACTCGCCAAGCCTTGTGCTCACAGGGCAAAG 1080
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Db       1021 TTAGGACTCCTTCAGTTCCTTTAGGACATACTCGCCAAGCCTTGTGCTCACAGGGCAAAG 1080

Qy       1081 GAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAATGATAAGATTTGATGTTTTTGCTT 1140
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Db       1081 GAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAATGATAAGATTTGATGTTTTTGCTT 1140

Qy       1141 GCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTCTGTAGCAGAAAACACGATAAAG 1200
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Db       1141 GCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTCTGTAGCAGAAAACACGATAAAG 1200

Qy       1201 CTATGATCTTTATTAGAG 1218
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Db       1201 CTATGATCTTTATTAGAG 1218
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RESULT 6
ACD42316
ID ACD42316 standard; cDNA; 1218 BP.
XX
AC ACD42316;
XX
DT 05-SEP-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO444 cDNA.
XX
KW Human; secreted and transmembrane protein; PRO; antidiabetic;
KW ophthalmological; cytostatic; immunostimulant; gene therapy;
KW vascular endothelial growth factor inhibitor; hypertrophy of adult heart;
KW protein secretion disorder; pancreas disorder; diabetes;
KW vascular permeability; retinal neuron cell survival; retinal disorder;
KW immune response; inflammation; mononuclear cell infiltration;
KW eosinophil infiltration; apoptosis; neoplastic growth; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003040014-A1.
XX
PD 27-FEB-2003.
XX
PF 01-FEB-2002; 2002US-00066269.
XX
PR 26-AUG-1997; 97US-0056974P.
PR 17-SEP-1997; 97US-0059115P.
PR 18-SEP-1997; 97US-0059263P.
PR 19-SEP-1997; 97US-0059588P.
PR 17-OCT-1997; 97US-0062285P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063082P.
PR 27-OCT-1997; 97US-0063329P.
PR 29-OCT-1997; 97US-0063733P.
PR 21-NOV-1997; 97US-0066364P.
PR 25-NOV-1997; 97US-0066840P.
PR 16-DEC-1997; 97US-0069694P.
PR 09-FEB-1998; 98US-0074086P.
PR 09-FEB-1998; 98US-0074092P.
PR 25-MAR-1998; 98US-0079294P.
PR 08-APR-1998; 98US-0081049P.
PR 14-JUL-1998; 98WO-US014552.
PR 10-AUG-1998; 98US-0095998P.
PR 18-AUG-1998; 98US-0097000P.
PR 09-SEP-1998; 98US-0099601P.
PR 10-SEP-1998; 98US-0099803P.
PR 10-SEP-1998; 98US-0099811P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 24-SEP-1998; 98US-0101922P.
PR 28-OCT-1998; 98US-0106032P.
PR 20-NOV-1998; 98US-0109304P.
PR 20-NOV-1998; 98WO-US024855.
PR 25-NOV-1998; 98WO-US025190.
PR 01-DEC-1998; 98WO-US025108.
PR 08-MAR-1999; 99WO-US005028.
PR 23-MAR-1999; 99US-0125778P.
PR 02-JUN-1999; 99WO-US012252.
PR 15-JUN-1999; 99US-0139695P.
PR 20-JUL-1999; 99US-0145070P.
PR 26-JUL-1999; 99US-0145698P.
PR 17-AUG-1999; 99US-0149396P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028565.
PR 07-DEC-1999; 99US-0169495P.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 09-MAR-2000; 2000WO-US006471.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 15-NOV-2001; 2001US-00002796.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
PI Wood WI, Zhang Z;
XX
DR WPI; 2003-503396/47.
DR P-PSDB; ABO25151.

```
XX
PT   New secreted and transmembrane PRO polypeptides, useful for treating
PT   diabetes, retinal disorders and stimulating an immune response.
XX
PS   Claim 2; Fig 3; 254pp; English.
XX
CC   The invention describes an isolated polypeptide (I) having at least 80 %
CC   amino acid sequence identity to 30 secreted and transmembrane
CC   polypeptides. PRO polypeptides are also useful for stimulating
CC   hypertrophy of adult heart, for inhibiting vascular endothelial growth
CC   factor stimulated proliferation of endothelial cells, stimulating
CC   proliferation of stimulated T-lymphocytes and for inducing proliferation
CC   of PDB12 pancreatic ductal cells and are thus useful in the treatment of
CC   disorders which involve protein secretion by the pancreas, including
CC   diabetes. PRO polypeptides are useful for inducing vascular permeability
CC   and in enhancing survival of retinal neurons cells and are thus useful
CC   for the treatment of retinal disorders. PRO polypeptides are also useful
CC   for stimulating an immune response and inducing inflammation by inducing
CC   mononuclear cell and eosinophil infiltration at the site of infection of
CC   an animal. The PRO polypeptides are further useful for inducing apoptosis
CC   in endothelial cells for inhibiting neoplastic growth. This sequence
CC   encodes a novel human secreted and transmembrane PRO polypeptide
XX
SQ   Sequence 1218 BP; 292 A; 299 C; 360 G; 267 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 1218;  DB 7;  Length 1218;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1218;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACA 60
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Db          1 CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACA 60

Qy         61 AAGGAGTCGCGCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGGAGTCGCGCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGT 120

Qy        121 CAGTGCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCT 180
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Db        121 CAGTGCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCT 180

Qy        181 GAGGGTTGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACC 240
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Db        181 GAGGGTTGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACC 240

Qy        241 GGACTGGGGCCGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAAC 300
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Db        241 GGACTGGGGCCGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAAC 300

Qy        301 CTGAGAAACAGCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTC 360
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Db        301 CTGAGAAACAGCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTC 360

Qy        361 CTAGAAGAGGGTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCC 420
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Db        361 CTAGAAGAGGGTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCC 420

Qy        421 CTTCTGAGGAGGCTGCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCT 480
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Db        421 CTTCTGAGGAGGCTGCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCT 480

Qy        481 GTAGTTGATAATGTTGGGAATAAGCTCTGCAACTTTCTTTGGCATTCAGTTGTTAAAAAC 540
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Db        481 GTAGTTGATAATGTTGGGAATAAGCTCTGCAACTTTCTTTGGCATTCAGTTGTTAAAAAC 540

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Db        601 TACCTAAATGATCGTCTTTGGTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGG 660

Qy        661 TCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTAC 720
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Db        661 TCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTAC 720

Qy        721 TACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACAC 780
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Db        721 TACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACAC 780

Qy        781 CCAACAGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACACAAGGAGCCAACCACG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CCAACAGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACACAAGGAGCCAACCACG 840

Qy        841 GGACCCTGTTCGGCCACCAAGGAGGGGCCGAGGACCTCATGAGCCAAGGAGAAAGAAACA 900
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Db        841 GGACCCTGTTCGGCCACCAAGGAGGGGCCGAGGACCTCATGAGCCAAGGAGAAAGAAACA 900

Qy        901 AAATGTGGATGGGCTAGTGTTGGACACACTGGCAGTAATACGGACTCTTGTAGATAAGTA 960
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Db        901 AAATGTGGATGGGCTAGTGTTGGACACACTGGCAGTAATACGGACTCTTGTAGATAAGTA 960

Qy        961 AGTATCTGACTCACGGTCACCTCCAGTGGAATGAAAAGTGTTCTGCCCGGAACCATGACT 1020
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Db        961 AGTATCTGACTCACGGTCACCTCCAGTGGAATGAAAAGTGTTCTGCCCGGAACCATGACT 1020

Qy       1021 TTAGGACTCCTTCAGTTCCTTTAGGACATACTCGCCAAGCCTTGTGCTCACAGGGCAAAG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTAGGACTCCTTCAGTTCCTTTAGGACATACTCGCCAAGCCTTGTGCTCACAGGGCAAAG 1080

Qy       1081 GAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAATGATAAGATTTGATGTTTTTGCTT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAATGATAAGATTTGATGTTTTTGCTT 1140

Qy       1141 GCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTCTGTAGCAGAAAACACGATAAAG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTCTGTAGCAGAAAACACGATAAAG 1200

Qy       1201 CTATGATCTTTATTAGAG 1218
              ||||||||||||||||||
Db       1201 CTATGATCTTTATTAGAG 1218


RESULT 7
ACA04925
ID   ACA04925 standard; cDNA; 1218 BP.
XX
AC   ACA04925;
XX
DT   28-MAY-2003  (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO444 cDNA.
XX
KW   Secreted and transmembrane polypeptide; PRO polypeptide; PRO533; PRO301;
KW   PRO187; PRO337; PRO1411; PRO10096; PRO246; PRO6307; PRO6003; PRO6004;
KW   PRO4356; PRO2630; PRO265; PRO941; FGFR; bioactive molecule;
KW   fibroblast growth factor receptor; cell death; chromosome mapping;
KW   gene mapping; transgenic animal; knockout animal; gene therapy; tumour;
KW   obesity; diabetes; insulinaemia; vascular permeability;
KW   cardiac insufficiency disorder; immune response; hearing loss;
KW   auditory hair cell regeneration; bone disorder; cartilage disorder;
KW   sports injury; arthritis; gène; ss.
XX
OS   Homo sapiens.
XX
PN   US2003032063-A1.
XX
PD   13-FEB-2003.
XX
PF   01-FEB-2002; 2002US-00066494.
XX
PR   26-AUG-1997;   97US-0056974P.
PR   17-SEP-1997;   97US-0059115P.
PR   18-SEP-1997;   97US-0059263P.
PR   19-SEP-1997;   97US-0059588P.
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PR 17-OCT-1997; 97US-0062285P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063082P.
PR 27-OCT-1997; 97US-0063329P.
PR 29-OCT-1997; 97US-0063733P.
PR 21-NOV-1997; 97US-0066364P.
PR 25-NOV-1997; 97US-0066840P.
PR 16-DEC-1997; 97US-0069694P.
PR 09-FEB-1998; 98US-0074086P.
PR 09-FEB-1998; 98US-0074092P.
PR 25-MAR-1998; 98US-0079294P.
PR 08-APR-1998; 98US-0081049P.
PR 10-AUG-1998; 98US-0095998P.
PR 18-AUG-1998; 98US-0097000P.
PR 09-SEP-1998; 98US-0099601P.
PR 10-SEP-1998; 98US-0099803P.
PR 10-SEP-1998; 98US-0099811P.
PR 10-SEP-1998; 98US-0099812P.
PR 14-SEP-1998; 98WO-US019093.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 24-SEP-1998; 98US-0101922P.
PR 28-OCT-1998; 98US-0106032P.
PR 20-NOV-1998; 98US-0109304P.
PR 20-NOV-1998; 98WO-US024855.
PR 25-NOV-1998; 98WO-US025190.
PR 01-DEC-1998; 98WO-US025108.
PR 08-MAR-1999; 99WO-US005028.
PR 23-MAR-1999; 99US-0125778P.
PR 02-JUN-1999; 99WO-US012252.
PR 15-JUN-1999; 99US-0139695P.
PR 20-JUL-1999; 99US-0145070P.
PR 26-JUL-1999; 99US-0145698P.
PR 17-AUG-1999; 99US-0149396P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028565.
PR 07-DEC-1999; 99US-0169495P.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 09-MAR-2000; 2000WO-US006471.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 15-NOV-2001; 2001US-00002796.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
PI Wood WI, Zhang Z;
XX
DR WPI; 2003-341964/32.
DR P-PSDB; ABU67269.
XX
PT Thirty seven nucleic acids encoding novel secreted and transmembrane PRO
PT polypeptides, useful for modulating biological activity of cell
PT expressing the polypeptide, and in chromosome and gene mapping.
XX
PS Claim 2; Fig 3; 255pp; English.
XX
CC The invention describes an isolated, secreted and transmembrane
CC polypeptide (I), termed PRO polypeptide. (I) Is useful for detecting
CC PRO533, PRO301, PRO187, PRO337, PRO1411, PRO10096, PRO246, PRO6307,
CC PRO6003, PRO6004, PRO4356, PRO2630, PRO265, PRO941, fibroblast growth
CC factor receptor (FGFR)-4, FGFR-3, FGFR-2 or FGFR-1 polypeptide, and for
CC linking a bioactive molecule e.g. toxin, radiolabel or antibody, to a
CC cell expressing the polypeptides. The bioactive molecule causes cell
CC death. (II) Is useful as hybridisation probes, in chromosome and gene
CC mapping, in generation of antisense RNA and DNA, in the preparation of
CC PRO polypeptide, for generating transgenic animals or knockout animals
CC which in turn are useful in the development and screening of
CC therapeutically useful reagents, and for the genetic analysis of
CC individuals with genetic disorders, in gene therapy, and for chromosome
CC identification. (I) Or Ab is useful for the preparation of medicament for
CC treating conditions which are responsive to the PRO polypeptide or anti-
CC PRO antibody e.g. a tumour. (I) is useful for treating obesity, diabetes
CC or hypo- or hyper-insulinaemia, and cardiac insufficiency disorders, for
CC inhibiting tumour growth, enhances vascular permeability and immune
CC response, for inducing regeneration of auditory hair cells and for
CC treating hearing loss in mammals, and for treating bone and/or cartilage
CC disorders such as sports injuries and arthritis. This sequence encodes a
CC novel human secreted and transmembrane polypeptide associated
CC oligonucleotide
XX
SQ Sequence 1218 BP; 292 A; 299 C; 360 G; 267 T; 0 U; 0 Other;

Query Match 100.0%; Score 1218; DB 7; Length 1218;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACA 60

Qy         61 AAGGAGTCGCGCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGGAGTCGCGCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGT 120

Qy        121 CAGTGCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCT 180
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Db        121 CAGTGCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCT 180

Qy        181 GAGGGTTGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACC 240
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Db        181 GAGGGTTGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACC 240

Qy        241 GGACTGGGGCCGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAAC 300
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Db        241 GGACTGGGGCCGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAAC 300

Qy        301 CTGAGAAACAGCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTGAGAAACAGCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTC 360

Qy        361 CTAGAAGAGGGTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTAGAAGAGGGTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCC 420

Qy        421 CTTCTGAGGAGGCTGCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCT 480
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Db        421 CTTCTGAGGAGGCTGCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCT 480

Qy        481 GTAGTTGATAATGTTGGGAATAAGCTCTGCAACTTTCTTTGGCATTCAGTTGTTAAAAAC 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTAGTTGATAATGTTGGGAATAAGCTCTGCAACTTTCTTTGGCATTCAGTTGTTAAAAAC 540

Qy        541 AAATAGGATGCAAATTCCTCAACTCCAGGTTATGAAAACAGTACTTGGAAAACTGAAAAC 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AAATAGGATGCAAATTCCTCAACTCCAGGTTATGAAAACAGTACTTGGAAAACTGAAAAC 600

Qy        601 TACCTAAATGATCGTCTTTGGTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGG 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TACCTAAATGATCGTCTTTGGTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGG 660

Qy        661 TCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTAC 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTAC 720

Qy        721 TACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACAC 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACAC 780

Qy        781 CCAACAGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACACAAGGAGCCAACCACG 840
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Db        781 CCAACAGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACACAAGGAGCCAACCACG 840

Qy        841 GGACCCTGTTCGGCCACCAAGGAGGGGCCGAGGACCTCATGAGCCAAGGAGAAAGAAACA 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGACCCTGTTCGGCCACCAAGGAGGGGCCGAGGACCTCATGAGCCAAGGAGAAAGAAACA 900

Qy        901 AAATGTGGATGGGCTAGTGTTGGACACACTGGCAGTAATACGGACTCTTGTAGATAAGTA 960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AAATGTGGATGGGCTAGTGTTGGACACACTGGCAGTAATACGGACTCTTGTAGATAAGTA 960

Qy        961 AGTATCTGACTCACGGTCACCTCCAGTGGAATGAAAAGTGTTCTGCCCCGGAACCATGACT 1020
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGTATCTGACTCACGGTCACCTCCAGTGGAATGAAAAGTGTTCTGCCCCGGAACCATGACT 1020

Qy       1021 TTAGGACTCCTTCAGTTCCTTTAGGACATACTCGCCAAGCCTTGTGCTCACAGGGCAAAG 1080
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTAGGACTCCTTCAGTTCCTTTAGGACATACTCGCCAAGCCTTGTGCTCACAGGGCAAAG 1080

Qy       1081 GAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAATGATAAGATTTGATGTTTTTGCTT 1140
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Db       1081 GAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAATGATAAGATTTGATGTTTTTGCTT 1140

Qy       1141 GCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTCTGTAGCAGAAAACACGATAAAG 1200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTCTGTAGCAGAAAACACGATAAAG 1200

Qy       1201 CTATGATCTTTATTAGAG 1218
                ||||||||||||||||||
Db       1201 CTATGATCTTTATTAGAG 1218
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RESULT 8
ACA60455
ID ACA60455 standard; cDNA; 1218 BP.
XX
AC ACA60455;
XX
DT 11-JUN-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO444 cDNA.
XX
KW Human; secreted and transmembrane polypeptide; PRO;
KW fibroblast growth factor receptor; PRO533; PRO301; PRO187; PRO337;
KW PRO1411; PRO10096; PRO246; PRO6307; PRO6003; FGFR-3; FGFR-4; FGFR-1;
KW FGFR-2; PRO6004; PRO4356; PRO2630; PRO265; PRO951; bioactive molecule;
KW toxin; radiolabel; antibody; cell death; chromosome mapping;
KW gene mapping; transgenic animal; knockout animal; gene therapy;
KW tissue typing; gene; ss.
XX
OS Homo sapiens.
XX
PN US2002177165-A1.
XX
PD 28-NOV-2002.
XX
PF 01-FEB-2002; 2002US-00066500.
XX
PR 26-AUG-1997; 97US-0056974P.
PR 17-SEP-1997; 97US-0059115P.
PR 18-SEP-1997; 97US-0059263P.
PR 19-SEP-1997; 97US-0059588P.
PR 17-OCT-1997; 97US-0062285P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063082P.
PR 27-OCT-1997; 97US-0063329P.
PR 29-OCT-1997; 97US-0063733P.
PR 21-NOV-1997; 97US-0066364P.
PR 25-NOV-1997; 97US-0066840P.
PR 16-DEC-1997; 97US-0069694P.
PR 09-FEB-1998; 98US-0074086P.
PR 09-FEB-1998; 98US-0074092P.
PR 25-MAR-1998; 98US-0079294P.
PR 08-APR-1998; 98US-0081049P.
PR 14-JUL-1998; 98WO-US014552.
PR 10-AUG-1998; 98US-0095998P.
PR 18-AUG-1998; 98US-0097000P.
PR 09-SEP-1998; 98US-0099601P.
PR 10-SEP-1998; 98US-0099803P.
PR 10-SEP-1998; 98US-0099811P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 24-SEP-1998; 98US-0101922P.
PR 28-OCT-1998; 98US-0106032P.
PR 20-NOV-1998; 98US-0109304P.
PR 20-NOV-1998; 98WO-US024855.
PR 25-NOV-1998; 98WO-US025190.
PR 01-DEC-1998; 98WO-US025108.
PR 08-MAR-1999; 99WO-US005028.
PR 23-MAR-1999; 99US-0125778P.
PR 02-JUN-1999; 99WO-US012252.
PR 15-JUN-1999; 99US-0139695P.
PR 20-JUL-1999; 99US-0145070P.
PR 26-JUL-1999; 99US-0145698P.
PR 17-AUG-1999; 99US-0149396P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028565.
PR 07-DEC-1999; 99US-0169495P.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 09-MAR-2000; 2000WO-US006471.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.

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PR   11-AUG-2000; 2000WO-US022031.
PR   23-AUG-2000; 2000WO-US023522.
PR   24-AUG-2000; 2000WO-US023328.
PR   01-DEC-2000; 2000WO-US032678.
PR   28-FEB-2001; 2001WO-US006520.
PR   30-MAY-2001; 2001WO-US017443.
PR   01-JUN-2001; 2001WO-US017800.
PR   20-JUN-2001; 2001WO-US019692.
PR   29-JUN-2001; 2001WO-US021066.
PR   09-JUL-2001; 2001WO-US021735.
PR   15-NOV-2001; 2001US-00002796.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Botstein DA,  Desnoyers L,  Eaton DL;
PI   Ferrara N,  Fong S,  Gao W,  Gerber H,  Gerritsen ME,  Goddard A;
PI   Godowski PJ,  Gurney AL,  Kljavin IJ,  Mather JP,  Napier MA,  Pan J;
PI   Paoni NF,  Roy MA,  Stewart TA,  Tumas D,  Watanabe CK,  Williams PM;
PI   Wood WI,  Zhang Z;
XX
DR   WPI; 2003-328482/31.
DR   P-PSDB; ABU72037.
XX
PT   Novel secreted and transmembrane polypeptide for modulating biological
PT   activity of cell expressing the polypeptide, for identifying agonists or
PT   antagonists of polypeptide, and as molecular weight markers.
XX
PS   Claim 2; Fig 3; 254pp; English.
XX
CC   The invention describes an isolated, secreted and transmembrane
CC   polypeptide (PP), termed PRO PP or fibroblast growth factor receptor PP
CC   (I). (I) is useful for detecting PRO533, PRO301, PRO187, PRO337, PRO1411,
CC   PRO10096, PRO246, PRO6307, PRO6003, fibroblast growth factor receptor
CC   (FGFR)-3, FGFR-4, FGFR-1, FGFR-2, PRO6004, PRO4356, PRO2630, PRO265 or
CC   PRO951 polypeptide, and for linking a bioactive molecule to a cell
CC   expressing the above polypeptides. The bioactive molecule, a toxin,
CC   radiolabel or an antibody, causes cell death. PRO is useful in assays to
CC   identify other proteins or molecules involved in binding interaction. The
CC   polynucleotide (II) encoding (I) is useful in chromosome and gene
CC   mapping, in generation of antisense RNA and DNA, for generating
CC   transgenic animals or knockout animals which in turn are useful in the
CC   development and screening of therapeutically useful reagents, to
CC   construct hybridisation probes for mapping the gene which encodes the PRO
CC   and for the genetic analysis of individuals with genetic disorders, in
CC   gene therapy, for chromosome identification and as a chromosome marker.
CC   (I) and (II) are useful for tissue typing. This sequence encodes a novel
CC   human secreted and transmembrane PRO polypeptide
XX
SQ   Sequence 1218 BP; 292 A; 299 C; 360 G; 267 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 1218;  DB 7;  Length 1218;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1218;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACA 60
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Db          1 CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACA 60

Qy         61 AAGGAGTCGCGCCGCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGT 120
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Db         61 AAGGAGTCGCGCCGCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGT 120

Qy        121 CAGTGCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCT 180
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Db        121 CAGTGCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCT 180

Qy        181 GAGGGTTGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACC 240
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Db        181 GAGGGTTGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACC 240

Qy        241 GGACTGGGGCCGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAAC 300
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Db        241 GGACTGGGGCCGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAAC 300

Qy        301 CTGAGAAACAGCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTC 360
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Db        301 CTGAGAAACAGCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTC 360

Qy        361 CTAGAAGAGGGTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCC 420
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Db        361 CTAGAAGAGGGTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCC 420

Qy        421 CTTCTGAGGAGGCTGCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTTCTGAGGAGGCTGCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCT 480

Qy        481 GTAGTTGATAATGTTGGGAATAAGCTCTGCAACTTTCTTTGGCATTCAGTTGTTAAAAAC 540
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Db        481 GTAGTTGATAATGTTGGGAATAAGCTCTGCAACTTTCTTTGGCATTCAGTTGTTAAAAAC 540

Qy        541 AAATAGGATGCAAATTCCTCAACTCCAGGTTATGAAAACAGTACTTGGAAAACTGAAAAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AAATAGGATGCAAATTCCTCAACTCCAGGTTATGAAAACAGTACTTGGAAAACTGAAAAC 600

Qy        601 TACCTAAATGATCGTCTTTGGTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TACCTAAATGATCGTCTTTGGTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGG 660

Qy        661 TCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTAC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTAC 720

Qy        721 TACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACAC 780

Qy        781 CCAACAGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACACAAGGAGCCAACCACG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CCAACAGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACACAAGGAGCCAACCACG 840

Qy        841 GGACCCTGTTCGGCCACCAAGGAGGGGCCGAGGACCTCATGAGCCAAGGAGAAAGAAACA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGACCCTGTTCGGCCACCAAGGAGGGGCCGAGGACCTCATGAGCCAAGGAGAAAGAAACA 900

Qy        901 AAATGTGGATGGGCTAGTGTTGGACACACTGGCAGTAATACGGACTCTTGTAGATAAGTA 960
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Db        901 AAATGTGGATGGGCTAGTGTTGGACACACTGGCAGTAATACGGACTCTTGTAGATAAGTA 960

Qy        961 AGTATCTGACTCACGGTCACCTCCAGTGGAATGAAAAGTGTTCTGCCCGGAACCATGACT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGTATCTGACTCACGGTCACCTCCAGTGGAATGAAAAGTGTTCTGCCCGGAACCATGACT 1020

Qy       1021 TTAGGACTCCTTCAGTTCCTTTAGGACATACTCGCCAAGCCTTGTGCTCACAGGGCAAAG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTAGGACTCCTTCAGTTCCTTTAGGACATACTCGCCAAGCCTTGTGCTCACAGGGCAAAG 1080

Qy       1081 GAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAATGATAAGATTTGATGTTTTTGCTT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAATGATAAGATTTGATGTTTTTGCTT 1140

Qy       1141 GCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTCTGTAGCAGAAAACACGATAAAG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTCTGTAGCAGAAAACACGATAAAG 1200

Qy       1201 CTATGATCTTTATTAGAG 1218
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Db       1201 CTATGATCTTTATTAGAG 1218


RESULT 9
ACA04445
ID   ACA04445 standard; cDNA; 1218 BP.
XX
AC   ACA04445;
XX
DT   28-MAY-2003  (first entry)
```

```
XX
DE   Novel human secreted and transmembrane protein PRO444 DNA.
XX
KW   Secreted and transmembrane polypeptide; PRO polypeptide; PRO533; PRO301;
KW   PRO187; PRO337; PRO1411; PRO10096; PRO246; PRO6307; PRO6003; PRO6004;
KW   PRO4356; PRO2630; PRO265; PRO941; FGFR; bioactive molecule;
KW   fibroblast growth factor receptor; cell death; chromosome mapping;
KW   gene mapping; transgenic animal; knockout animal; gene therapy; tumour;
KW   obesity; diabetes; insulinaemia; vascular permeability;
KW   cardiac insufficiency disorder; immune response; hearing loss;
KW   auditory hair cell regeneration; bone disorder; cartilage disorder;
KW   sports injury; arthritis; gene; ss.
XX
OS   Homo sapiens.
XX
PN   US2003032062-A1.
XX
PD   13-FEB-2003.
XX
PF   01-FEB-2002; 2002US-00066273.
XX
PR   26-AUG-1997;   97US-0056974P.
PR   17-SEP-1997;   97US-0059115P.
PR   18-SEP-1997;   97US-0059263P.
PR   19-SEP-1997;   97US-0059588P.
PR   17-OCT-1997;   97US-0062285P.
PR   24-OCT-1997;   97US-0062816P.
PR   24-OCT-1997;   97US-0063082P.
PR   27-OCT-1997;   97US-0063329P.
PR   29-OCT-1997;   97US-0063733P.
PR   21-NOV-1997;   97US-0066364P.
PR   25-NOV-1997;   97US-0066840P.
PR   16-DEC-1997;   97US-0069694P.
PR   09-FEB-1998;   98US-0074086P.
PR   09-FEB-1998;   98US-0074092P.
PR   25-MAR-1998;   98US-0079294P.
PR   08-APR-1998;   98US-0081049P.
PR   14-JUL-1998;   98WO-US014552.
PR   10-AUG-1998;   98US-0095998P.
PR   18-AUG-1998;   98US-0097000P.
PR   09-SEP-1998;   98US-0099601P.
PR   10-SEP-1998;   98US-0099803P.
PR   10-SEP-1998;   98US-0099811P.
PR   10-SEP-1998;   98US-0099812P.
PR   10-SEP-1998;   98WO-US018824.
PR   14-SEP-1998;   98WO-US019093.
PR   16-SEP-1998;   98WO-US019330.
PR   17-SEP-1998;   98US-0100858P.
PR   17-SEP-1998;   98WO-US019437.
PR   24-SEP-1998;   98US-0101922P.
PR   28-OCT-1998;   98US-0106032P.
PR   20-NOV-1998;   98US-0109304P.
PR   20-NOV-1998;   98WO-US024855.
PR   25-NOV-1998;   98WO-US025190.
PR   01-DEC-1998;   98WO-US025108.
PR   08-MAR-1999;   99WO-US005028.
PR   23-MAR-1999;   99US-0125778P.
PR   02-JUN-1999;   99WO-US012252.
PR   15-JUN-1999;   99US-0139695P.
PR   20-JUL-1999;   99US-0145070P.
PR   26-JUL-1999;   99US-0145698P.
PR   17-AUG-1999;   99US-0149396P.
PR   01-SEP-1999;   99WO-US020111.
PR   08-SEP-1999;   99WO-US020594.
PR   15-SEP-1999;   99WO-US021090.
PR   15-SEP-1999;   99WO-US021547.
PR   30-NOV-1999;   99WO-US028313.
PR   01-DEC-1999;   99WO-US028301.
PR   02-DEC-1999;   99WO-US028565.
PR   07-DEC-1999;   99US-0169495P.
PR   20-DEC-1999;   99WO-US030999.
PR   05-JAN-2000; 2000WO-US000219.
PR   18-FEB-2000; 2000WO-US004341.
PR   18-FEB-2000; 2000WO-US004342.
PR   22-FEB-2000; 2000WO-US004414.
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005841.
PR   09-MAR-2000; 2000WO-US006471.
PR   20-MAR-2000; 2000WO-US007377.
PR   30-MAR-2000; 2000WO-US008439.
PR   15-MAY-2000; 2000WO-US013358.
PR   17-MAY-2000; 2000WO-US013705.
PR   22-MAY-2000; 2000WO-US014042.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US015264.
PR   11-AUG-2000; 2000WO-US022031.
PR   23-AUG-2000; 2000WO-US023522.
PR   24-AUG-2000; 2000WO-US023328.
PR   01-DEC-2000; 2000WO-US032678.
PR   28-FEB-2001; 2001WO-US006520.
PR   30-MAY-2001; 2001WO-US017443.
PR   01-JUN-2001; 2001WO-US017800.
PR   20-JUN-2001; 2001WO-US019692.
PR   29-JUN-2001; 2001WO-US021066.
PR   09-JUL-2001; 2001WO-US021735.
PR   15-NOV-2001; 2001US-00002796.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Botstein DA,  Desnoyers L,  Eaton DL;
PI   Ferrara N,  Fong S,  Gao W,  Gerber H,  Gerritsen ME,  Goddard A;
PI   Godowski PJ,  Gurney AL,  Kljavin IJ,  Mather JP,  Napier MA,  Pan J;
PI   Paoni NF,  Roy MA,  Stewart TA,  Tumas D,  Watanabe CK,  Williams PM;
PI   Wood WI,  Zhang Z;
XX
DR   WPI; 2003-341963/32.
DR   P-PSDB; ABU67138.
XX
PT   New secreted and transmembrane polypeptide for modulating biological
PT   activity of a cell expressing the polypeptide, identifying agonists or
PT   antagonists of the polypeptide, and as molecular weight markers.
XX
PS   Claim 2; Fig 3; 254pp; English.
XX
CC   The invention describes an isolated, secreted and transmembrane
CC   polypeptide (I), termed PRO polypeptide. (I) Is useful for detecting
CC   PRO533, PRO301, PRO187, PRO337, PRO1411, PRO10096, PRO246, PRO6307,
CC   PRO6003, PRO6004, PRO4356, PRO2630, PRO265, PRO941, fibroblast growth
CC   factor receptor (FGFR)-4, FGFR-3, FGFR-2 or FGFR-1 polypeptide, and for
CC   linking a bioactive molecule e.g. toxin, radiolabel or antibody, to a
CC   cell expressing the polypeptides. The bioactive molecule causes cell
CC   death. (II) Is useful as hybridisation probes, in chromosome and gene
CC   mapping, in generation of antisense RNA and DNA, in the preparation of
CC   PRO polypeptide, for generating transgenic animals or knockout animals
CC   which in turn are useful in the development and screening of
CC   therapeutically useful reagents, and for the genetic analysis of
CC   individuals with genetic disorders, in gene therapy, and for chromosome
CC   identification. (I) Or Ab is useful for the preparation of medicament for
CC   treating conditions which are responsive to the PRO polypeptide or anti-
CC   PRO antibody e.g. a tumour. (I) is useful for treating obesity, diabetes
CC   or hypo- or hyper-insulinaemia, and cardiac insufficiency disorders, for
CC   inhibiting tumour growth, enhances vascular permeability and immune
CC   response, for inducing regeneration of auditory hair cells and for
CC   treating hearing loss in mammals, and for treating bone and/or cartilage
CC   disorders such as sports injuries and arthritis. This sequence encodes a
CC   novel human secreted and transmembrane polypeptide
XX
SQ   Sequence 1218 BP; 292 A; 299 C; 360 G; 267 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 1218;  DB 7;  Length 1218;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1218;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACA 60
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Db          1 CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACA 60
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Qy        61 AAGGAGTCGCGCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGT 120
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Qy       121 CAGTGCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCT 180
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Db       121 CAGTGCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCT 180

Qy       181 GAGGGTTGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACC 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 GAGGGTTGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACC 240

Qy       241 GGACTGGGGCCGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAAC 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 GGACTGGGGCCGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAAC 300

Qy       301 CTGAGAAACAGCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTC 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 CTGAGAAACAGCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTC 360

Qy       361 CTAGAAGAGGGTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCC 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 CTAGAAGAGGGTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCC 420

Qy       421 CTTCTGAGGAGGCTGCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCT 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 CTTCTGAGGAGGCTGCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCT 480

Qy       481 GTAGTTGATAATGTTGGGAATAAGCTCTGCAACTTTCTTTGGCATTCAGTTGTTAAAAAC 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 GTAGTTGATAATGTTGGGAATAAGCTCTGCAACTTTCTTTGGCATTCAGTTGTTAAAAAC 540

Qy       541 AAATAGGATGCAAATTCCTCAACTCCAGGTTATGAAAACAGTACTTGGAAAACTGAAAAC 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 AAATAGGATGCAAATTCCTCAACTCCAGGTTATGAAAACAGTACTTGGAAAACTGAAAAC 600

Qy       601 TACCTAAATGATCGTCTTTGGTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGG 660
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Db       601 TACCTAAATGATCGTCTTTGGTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGG 660

Qy       661 TCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTAC 720
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Qy       721 TACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACAC 780
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Db       721 TACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACAC 780

Qy       781 CCAACAGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACACAAGGAGCCAACCACG 840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 CCAACAGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACACAAGGAGCCAACCACG 840

Qy       841 GGACCCTGTTCGGCCACCAAGGAGGGGCCGAGGACCTCATGAGCCAAGGAGAAAGAAACA 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 GGACCCTGTTCGGCCACCAAGGAGGGGCCGAGGACCTCATGAGCCAAGGAGAAAGAAACA 900

Qy       901 AAATGTGGATGGGCTAGTGTTGGACACACTGGCAGTAATACGGACTCTTGTAGATAAGTA 960
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Db       901 AAATGTGGATGGGCTAGTGTTGGACACACTGGCAGTAATACGGACTCTTGTAGATAAGTA 960

Qy       961 AGTATCTGACTCACGGTCACCTCCAGTGGAATGAAAAGTGTTCTGCCCGGAACCATGACT 1020
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Db       961 AGTATCTGACTCACGGTCACCTCCAGTGGAATGAAAAGTGTTCTGCCCGGAACCATGACT 1020

Qy      1021 TTAGGACTCCTTCAGTTCCTTTAGGACATACTCGCCAAGCCTTGTGCTCACAGGGCAAAG 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 TTAGGACTCCTTCAGTTCCTTTAGGACATACTCGCCAAGCCTTGTGCTCACAGGGCAAAG 1080

Qy      1081 GAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAATGATAAGATTTGATGTTTTTGCTT 1140
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Db      1081 GAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAATGATAAGATTTGATGTTTTTGCTT 1140

Qy      1141 GCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTCTGTAGCAGAAAACACGATAAAG 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 GCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTCTGTAGCAGAAAACACGATAAAG 1200

Qy      1201 CTATGATCTTTATTAGAG 1218
             ||||||||||||||||||
Db      1201 CTATGATCTTTATTAGAG 1218
```

RESULT 10
ACA65586
ID ACA65586 standard; cDNA; 1218 BP.
XX
AC ACA65586;
XX
DT 19-JUN-2003 (first entry)
XX
DE Human cDNA *encoding* secreted/transmembrane protein PRO444.
XX
KW Human; ss; gene; secreted protein; transmembrane protein; PRO;
KW genetic disorder; gene therapy.
XX
OS Homo sapiens.
XX
PN US2003032057-A1.
XX
PD 13-FEB-2003.
XX
PF 15-NOV-2001; 2001US-00002796.
XX
PR 26-AUG-1997; 97US-0056974P.
PR 17-SEP-1997; 97US-0059115P.
PR 18-SEP-1997; 97US-0059263P.
PR 19-SEP-1997; 97US-0059588P.
PR 17-OCT-1997; 97US-0062285P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063082P.
PR 27-OCT-1997; 97US-0063329P.
PR 29-OCT-1997; 97US-0063733P.
PR 21-NOV-1997; 97US-0066364P.
PR 25-NOV-1997; 97US-0066840P.
PR 16-DEC-1997; 97US-0069694P.
PR 09-FEB-1998; 98US-0074086P.
PR 09-FEB-1998; 98US-0074092P.
PR 25-MAR-1998; 98US-0079294P.
PR 08-APR-1998; 98US-0081049P.
PR 14-JUL-1998; 98WO-US014552.
PR 10-AUG-1998; 98US-0095998P.
PR 18-AUG-1998; 98US-0097000P.
PR 09-SEP-1998; 98US-0099601P.
PR 10-SEP-1998; 98US-0099803P.
PR 10-SEP-1998; 98US-0099811P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 24-SEP-1998; 98US-0101922P.
PR 28-OCT-1998; 98US-0106032P.
PR 20-NOV-1998; 98US-0109304P.
PR 20-NOV-1998; 98WO-US024855.
PR 25-NOV-1998; 98WO-US025190.
PR 01-DEC-1998; 98WO-US025108.
PR 08-MAR-1999; 99WO-US005028.
PR 23-MAR-1999; 99US-0125778P.
PR 02-JUN-1999; 99WO-US012252.
PR 15-JUN-1999; 99US-0139695P.
PR 20-JUL-1999; 99US-0145070P.
PR 26-JUL-1999; 99US-0145698P.
PR 17-AUG-1999; 99US-0149396P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.

PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028565.
PR 07-DEC-1999; 99US-0169495P.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 09-MAR-2000; 2000WO-US006471.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
PI Wood WI, Zhang Z;
XX
DR WPI; 2003-341960/32.
DR P-PSDB; ABU79780.
XX
PT Novel secreted and transmembrane polypeptide for modulating biological
PT activity of cell expressing the polypeptide, identifying agonists or
PT antagonists of polypeptide, and as molecular weight markers.
XX
PS Claim 2; Fig 3; 255pp; English.
XX
CC The invention relates to an isolated, secreted/transmembrane polypeptide,
CC termed PRO polypeptide, having at least 80% sequence identity to a
CC sequence selected from any one of the 37 sequences appearing as ABU79779
CC -ABU79815 or to a sequence encoded by a nucleic acid molecule deposited
CC under any one of the ATCC numbers given in the specification. Also
CC included are an isolated nucleic acid molecule having at least 80%
CC sequence identity to a sequence selected from any one of the 37 cDNA
CC sequences defined in the specification (or encoding the mature PRO
CC protein or a PRO protein extracellular domain), a PRO expression vector,
CC a hoist cell comprising the vector, PRO fusion proteins, anti-PRO
CC antibodies and a method for linking a bioactive molecule to a cell
CC expressing the above PRO polypeptides, the bioactive molecule is a toxin,
CC radiolabel or an antibody and causes the death of the cell. PRO or the
CC antibody is useful for modulating at least one biological activity of
CC cell expressing the above polypeptides. PRO is useful for identifying
CC agonists or antagonists of PRO, for preparing a variant of PRO, as
CC molecular weight markers for protein electrophoresis purpose and PRO
CC nucleic acid is useful for recombinantly expressing those markers. PRO is
CC also useful as therapeutic agent. PRO is useful in assays to identify
CC other proteins or molecules involved in binding interaction. PRO nucleic
CC acid is useful as hybridisation probes, in chromosome and gene mapping,
CC in generation of antisense RNA and DNA, in the preparation of PRO
CC polypeptide, in gene therapy, for generating transgenic animals or
CC knockout animals which in turn are useful in the development and
CC screening of therapeutically useful reagents, to construct hybridisation
CC probes for mapping the gene which encodes the PRO and for the genetic
CC analysis of individuals with genetic disorders, for chromosome
CC identification, as a chromosome marker, and for generating probes for
CC polymerase chain reaction (PCR), Northern analysis, Southern analysis and
CC Western analysis. The antibody is useful in diagnostic assays for PRO,
CC e.g. detecting its expression in specific cells, tissues or serum, for
CC affinity purification of PRO from recombinant cell culture or natural
CC sources. PRO or Ab is useful for the preparation of medicament for
CC treating conditions which is responsive to the PRO polypeptide or anti-
CC PRO antibody. PRO and PRO nucleic acid are useful for tissue typing. The
CC present sequence encodes a PRO polypeptide
XX
SQ Sequence 1218 BP; 292 A; 299 C; 360 G; 267 T; 0 U; 0 Other;

Query Match 100.0%; Score 1218; DB 8; Length 1218;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACA 60
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Qy         61 AAGGAGTCGCGCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGGAGTCGCGCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGT 120

Qy        121 CAGTGCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCT 180
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Db        121 CAGTGCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCT 180

Qy        181 GAGGGTTGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACC 240
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Qy        241 GGACTGGGGCCGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAAC 300
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Qy        301 CTGAGAAACAGCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTC 360
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RESULT 11
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XX
AC ACD68242;
XX
DT 17-SEP-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO444 cDNA.
XX
KW Human; secreted and transmembrane protein; PRO; angiogenesis;
KW endothelial cell proliferation; wound healing; immune response;
KW T-lymphocytes proliferation; neonatal heart hypertrophy; tumour;
KW cardiac insufficiency disorder; calcium flux; inflammation;
KW vascular endothelial growth factor-stimulated proliferation;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW nephropathy; Schanlein-Henoch purpura; celiac disease; Crohn's disease;
KW dermatitis herpetiformis; diabetes; haemoglobin switch; insulinaemia;
KW pancreatic beta-cell precursor cell differentiation; thalassemias;
KW obesity; auditory hair cell regeneration; hearing loss; bone disorder;
KW cartilage disorder; sports injury; arthritis; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003073130-A1.
XX
PD 17-APR-2003.
XX
PF 11-DEC-2001; 2001US-00015869.
XX
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PR   09-JUL-2001; 2001WO-US021735.
PR   04-SEP-2001; 2001US-00946374.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Botstein D,  Desnoyers L,  Eaton DL,  Ferrara N,  Fong S;
PI   Gao W,  Goddard A,  Godowski PJ,  Grimaldi JC,  Gurney AL,  Hillan KJ;
PI   Pan J,  Paoni NF,  Roy MA,  Smith V,  Stewart TA,  Tumas D,  Watanabe CK;
PI   Williams PM,  Wood WI;
XX
DR   WPI; 2003-585293/55.
DR   P-PSDB; ABO33583.
XX
PT   Novel isolated PRO polypeptides e.g. PRO1130, PRO1275, PRO1418, PRO1555,
PT   PRO1787 that modulate glucose or free fatty acid uptake by skeletal
PT   muscle cells, and are useful for treating diabetes, hyper- or hypo-

  Query Match           100.0%;  Score 1218;  DB 8;  Length 1218;
  Best Local Similarity  100.0%;  Pred. No. 0;
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Qy          1 CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACA 60
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RESULT 12
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ID ADA47180 standard; cDNA; 1218 BP.
XX
AC ADA47180;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human secreted/transmembrane polypeptide PRO444 cDNA.
XX
KW human; ss; gene; secreted protein; transmembrane protein; PRO;
KW VEGF inhibitor; vascular endothelial growth factor;
KW endothelial cell proliferation; T-lymphocyte proliferation;
KW endothelial cell apoptosis; c-fos stimulation;
KW pancreatic beta cell differentiation; chondrocyte proliferation;
KW glucose uptake; free fatty acid; FFA uptake; tissue typing.
XX
OS Homo sapiens.
XX
PN US2003044844-A1.
XX
PD 06-MAR-2003.
XX
PF 01-FEB-2002; 2002US-00066211.
XX
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PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
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PR 09-MAR-2000; 2000WO-US006471.
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PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 11-AUG-2000; 2000WO-US022031.
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PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 15-NOV-2001; 2001US-00002796.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
PI Wood WI, Zhang Z;
XX
DR WPI; 2003-615775/58.
DR P-PSDB; ADA47181.
XX
PT Novel isolated PRO polypeptides e.g. PRO365 and PRO187, useful for
PT inducing redifferentiation and/or proliferation of chondrocytes, and for
PT modulating glucose or free fatty acid uptake by skeletal muscle cells.

XX
PS Claim 1; Fig 4; 254pp; English.
XX
CC The invention relates to an isolated secreted/transmembrane PRO
CC polypeptide. The polypeptide and its nucleic acid is useful as an
CC inhibitor of vascular endothelial growth factor stimulated proliferation
CC of endothelial cells, as a stimulator of T-lymphocyte proliferation, as
CC an inducer of endothelial cell apoptosis, c-fos and differentiation of
CC pancreatic beta cell precursors into mature cell, for induction of
CC redifferentiation and/or proliferation of chondrocytes and for modulating
CC glucose or free fatty acid (FFA) uptake by skeletal muscle cells. The
CC polypeptide and its nucleic acid is useful for generating transgenic or
CC knock-out animals, for tissue typing and for chromosome identification.
CC The polypeptide is useful in a number of functional biological assays, as
CC molecular weight marker for protein electrophoresis, and as therapeutic
CC agents. The nucleic acid is useful as a hybridisation probe, in
CC chromosome and gene mapping, in the generation of antisense RNA and DNA,
CC and for the preparation PRO polypeptides. The nucleic acid is also useful
CC as hybridisation probe for a cDNA library to isolate the full length PRO
CC cDNA, to isolate other cDNA and in gene therapy. The nucleic acid is also
CC useful in the construction of hybridisation probes for mapping the gene
CC encoding PRO, and for the genetic analysis of individuals with the
CC genetic disorders. The present sequence represents a cDNA encoding a
CC human secreted/transmembrane PRO polypeptide.
XX
SQ Sequence 1218 BP; 292 A; 299 C; 360 G; 267 T; 0 U; 0 Other;

Query Match 100.0%; Score 1218; DB 8; Length 1218;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       1201 CTATGATCTTTATTAGAG 1218
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RESULT 13
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XX
AC ACH04344;
XX
DT 01-OCT-2003 (first entry)
XX
DE Human cDNA encoding secreted/transmembrane protein PRO444.
XX
KW Human; ss; gene; secreted protein; transmembrane protein; PRO; vulnerary;
KW cardiant; antidiabetic; anorectic; antiarthritic; angiogenesis; cancer;
KW adrenal cortical capillary; endothelial cell growth; wound healing;
KW stimulated T-lymphocyte proliferation; immune response suppression;
KW neonatal heart hypertrophy; cardiac insufficiency disorder;
KW vascular endothelial growth factor; inflammation; mononuclear cell;
KW eosinophil; diabetes; obesity; or hyper-insulinaemia; hypo-insulinaemia;
KW chondrocyte redifferentiation; bone disorder; cartilage disorder;
KW sports injury; arthritis.
XX
OS Homo sapiens.
XX
PN US2003044841-A1.
XX
PD 06-MAR-2003.
XX
PF 06-DEC-2001; 2001US-00006856.
XX
PR 01-SEP-1998; 98US-0098716P.
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PR 16-APR-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
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PR 15-SEP-1999; 99WO-US021194.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
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PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
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PR 22-MAY-2000; 2000WO-US014042.
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PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
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DR WPI; 2003-492259/46.
DR P-PSDB; ABO44436.
XX
PT Novel secreted and transmembrane polypeptides and polynucleotides
PT encoding them useful for treating various cardiac insufficiency
PT disorders, bone and/or cartilage disorders such as sports injuries and
PT arthritis.

Query Match 100.0%; Score 1218; DB 8; Length 1218;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACA 60
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Qy        721 TACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACAC 780
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Db        721 TACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACAC 780

Qy        781 CCAACAGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACACAAGGAGCCAACCACG 840
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Db        781 CCAACAGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACACAAGGAGCCAACCACG 840

Qy        841 GGACCCTGTTCGGCCACCAAGGAGGGGCCGAGGACCTCATGAGCCAAGGAGAAAGAAACA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGACCCTGTTCGGCCACCAAGGAGGGGCCGAGGACCTCATGAGCCAAGGAGAAAGAAACA 900

Qy        901 AAATGTGGATGGGCTAGTGTTGGACACACTGGCAGTAATACGGACTCTTGTAGATAAGTA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AAATGTGGATGGGCTAGTGTTGGACACACTGGCAGTAATACGGACTCTTGTAGATAAGTA 960

Qy        961 AGTATCTGACTCACGGTCACCTCCAGTGGAATGAAAAGTGTTCTGCCCGGAACCATGACT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGTATCTGACTCACGGTCACCTCCAGTGGAATGAAAAGTGTTCTGCCCGGAACCATGACT 1020

Qy       1021 TTAGGACTCCTTCAGTTCCTTTAGGACATACTCGCCAAGCCTTGTGCTCACAGGGCAAAG 1080
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Db       1021 TTAGGACTCCTTCAGTTCCTTTAGGACATACTCGCCAAGCCTTGTGCTCACAGGGCAAAG 1080

Qy       1081 GAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAATGATAAGATTTGATGTTTTTGCTT 1140
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Db       1081 GAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAATGATAAGATTTGATGTTTTTGCTT 1140

Qy       1141 GCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTCTGTAGCAGAAAACACGATAAAG 1200
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Db       1141 GCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTCTGTAGCAGAAAACACGATAAAG 1200

Qy       1201 CTATGATCTTTATTAGAG 1218
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Db       1201 CTATGATCTTTATTAGAG 1218
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RESULT 14
ACD67888
ID ACD67888 standard; cDNA; 1218 BP.
XX
AC ACD67888;
XX
DT 17-SEP-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO444 cDNA.
XX
KW Human; secreted and transmembrane protein; PRO; gene therapy; vaccine;
KW tissue typing; chromosome identification; vaccine; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003073129-A1.
XX
PD 17-APR-2003.
XX
PF 04-SEP-2001; 2001US-00946374.
XX
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 01-SEP-1998; 98US-0098749P.
PR 01-SEP-1998; 98US-0098750P.
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PR 22-OCT-1998; 98US-0105169P.
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PR 26-OCT-1998; 98US-0105693P.
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PR 29-OCT-1998; 98US-0106384P.
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PR 03-NOV-1998; 98US-0106856P.
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PR 03-NOV-1998; 98US-0106934P.
PR 10-NOV-1998; 98US-0107783P.
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PR 17-NOV-1998; 98US-0108779P.
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PR 17-NOV-1998; 98US-0108925P.
PR 18-NOV-1998; 98US-0108848P.
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PR 18-NOV-1998; 98US-0108850P.
PR 18-NOV-1998; 98US-0108851P.
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PR 18-NOV-1998; 98US-0108904P.
PR 22-DEC-1998; 98US-00218517.
PR 22-DEC-1998; 98US-0113296P.
PR 30-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 99WO-US000106.
PR 12-APR-1999; 99US-00284291.
PR 16-APR-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021194.
PR 18-OCT-1999; 99US-00403297.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.

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PR   01-MAR-2001; 2001WO-US006666.
PR   01-JUN-2001; 2001US-00872035.
PR   01-JUN-2001; 2001WO-US017800.
PR   14-JUN-2001; 2001US-00882636.
PR   20-JUN-2001; 2001WO-US019692.
PR   29-JUN-2001; 2001WO-US021066.
PR   09-JUL-2001; 2001WO-US021735.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI   Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI   Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI   Williams PM, Wood WI;
XX
DR   WPI; 2003-585292/55.
DR   P-PSDB; ABO33460.
XX
PT   Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful in the
PT   preparation of a medicament for treating a condition responsive to PRO
PT   polypeptide, and as therapeutic agents e.g. vaccines.
XX
PS   Claim 2; Fig 3; 561pp; English.
XX
CC   The invention describes an isolated PRO (secreted and transmembrane)
CC   polypeptide (I), having at least 80% sequence identity to a sequence

  Query Match           100.0%;  Score 1218;  DB 8;  Length 1218;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1218;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACA 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACA 60

Qy       61 AAGGAGTCGCGCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGT 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 AAGGAGTCGCGCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGT 120

Qy      121 CAGTGCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCT 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 CAGTGCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCT 180

Qy      181 GAGGGTTGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACC 240
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Qy      241 GGACTGGGGCCGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAAC 300
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Qy      301 CTGAGAAACAGCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTC 360
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Db      301 CTGAGAAACAGCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTC 360

Qy      361 CTAGAAGAGGGTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCC 420
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Db      361 CTAGAAGAGGGTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCC 420

Qy      421 CTTCTGAGGAGGCTGCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCT 480
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Qy      481 GTAGTTGATAATGTTGGGAATAAGCTCTGCAACTTTCTTTGGCATTCAGTTGTTAAAAAC 540
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Qy      541 AAATAGGATGCAAATTCCTCAACTCCAGGTTATGAAAACAGTACTTGGAAAACTGAAAAC 600
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Qy      721 TACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACAC 780
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Db      721 TACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACAC 780

Qy      781 CCAACAGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACACAAGGAGCCAACCACG 840
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Db      781 CCAACAGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACACAAGGAGCCAACCACG 840

Qy      841 GGACCCTGTTCGGCCACCAAGGAGGGGCCGAGGACCTCATGAGCCAAGGAGAAAGAAACA 900
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Db      841 GGACCCTGTTCGGCCACCAAGGAGGGGCCGAGGACCTCATGAGCCAAGGAGAAAGAAACA 900

Qy      901 AAATGTGGATGGGCTAGTGTTGGACACACTGGCAGTAATACGGACTCTTGTAGATAAGTA 960
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Qy      961 AGTATCTGACTCACGGTCACCTCCAGTGGAATGAAAAGTGTTCTGCCCGGAACCATGACT 1020
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Db      961 AGTATCTGACTCACGGTCACCTCCAGTGGAATGAAAAGTGTTCTGCCCGGAACCATGACT 1020

Qy     1021 TTAGGACTCCTTCAGTTCCTTTAGGACATACTCGCCAAGCCTTGTGCTCACAGGGCAAAG 1080
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Qy     1081 GAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAATGATAAGATTTGATGTTTTTGCTT 1140
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Qy     1201 CTATGATCTTTATTAGAG 1218
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Db     1201 CTATGATCTTTATTAGAG 1218


RESULT 15
ACD30202
ID   ACD30202 standard; cDNA; 1218 BP.
XX
AC   ACD30202;
XX
DT   29-AUG-2003  (first entry)
XX
DE   Human cDNA encoding Pro444.
XX
KW   Human; ss; gene; PRO; secreted and transmembrane protein; gene therapy;
KW   enterocolitis; gastrointestinal ulceration; skin disease; asthma;
KW   abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
KW   squamous cell carcinoma; Alzheimer's disease; Parkinson's disease;
KW   amyotrophic lateral sclerosis; inflammatory disease; organ failure;
KW   rheumatoid arthritis; multiple sclerosis; atherosclerosis; infertility;
KW   cardiac injury; birth defect; premature aging; AIDS; cancer;
KW   diabetic complication; wound repair.
XX
OS   Homo sapiens.
XX
PN   US2003044902-A1.
XX
PD   06-MAR-2003.
XX
PF   01-FEB-2002; 2002US-00066193.
XX
PR   26-AUG-1997;   97US-0056974P.
PR   17-SEP-1997;   97US-0059115P.
PR   18-SEP-1997;   97US-0059263P.
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PR 08-MAR-1999; 99WO-US005028.
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PR 02-JUN-1999; 99WO-US012252.
PR 15-JUN-1999; 99US-0139695P.
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PR 26-JUL-1999; 99US-0145698P.
PR 17-AUG-1999; 99US-0149396P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028565.
PR 07-DEC-1999; 99US-0169495P.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 09-MAR-2000; 2000WO-US006471.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 15-NOV-2001; 2001US-00002796.
XX
PA (GETH) GENENTECH INC.
XX

PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
PI Wood WI, Zhang Z;
XX
DR WPI; 2003-492261/46.
DR P-PSDB; ABO19838.
XX
PT New PRO polypeptides and nucleic acid molecules, useful in diagnosing or
PT treating inflammatory diseases, organ failure, atherosclerosis, cardiac
PT injury, infertility, cancer, AIDS, Alzheimer's disease or Parkinson's
PT disease.
XX
PS Claim 3; Fig 3; 154pp; English.
XX
CC The invention relates to an isolated native sequence PRO polypeptide
CC (secreted and transmembrane protein) having 80% sequence similarity to
CC one of 37 proteins sequences (or PRO lacking its signal peptide, a PRO
CC extracellular domain (with or without a signal peptide) encoded by a
CC nucleic acids 80% identical to one of 37 cDNA sequences, shown in the
CC specification. Also included are vectors comprising the PRO nucleic
CC acids, host cells comprising the vectors (used to produce the PRO
CC proteins), a chimaeric molecule comprising the PRO polypeptide fused to a
CC heterologous amino acid sequence, an anti-PRO antibody, linking a
CC bioactive molecule to a cell expressing the PRO polypeptides and
CC modulating at least one biological activity of a cell expressing the
CC polypeptides. The PRO polypeptides and nucleic acids are useful in
CC diagnosing or treating enterocolitis, gastrointestinal ulceration, skin
CC diseases associated with abnormal keratinocyte differentiation, e.g.
CC psoriasis or epithelial cancers such as squamous cell carcinoma,
CC Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis,
CC inflammatory diseases, e.g. rheumatoid arthritis, asthma or multiple
CC sclerosis, organ failure, atherosclerosis, cardiac injury, infertility,
CC birth defects, premature aging, AIDS, cancer, diabetic complications, or
CC mutations in general. The polypeptides are also useful for wound repair
CC and associated therapies concerned with re-growth of tissue. The
CC nucleotide sequences may be used as hybridisation probes in chromosome
CC and gene mapping, or in generating antisense RNA and DNA. PRO nucleic
CC acids are also useful in preparing PRO polypeptides, in assays to
CC identify other proteins or molecules involved in binding reaction, to
CC generate transgenic animals or knockout animals, which in turn are useful
CC in the development and screening of therapeutically useful reagents, for
CC chromosome identification, and tissue typing. The PRO polypeptides and
CC nucleic acid molecules are also useful in gene therapy, and as molecular
CC weight markers for protein electrophoresis purposes. The anti-PRO
CC antibodies may be used in diagnostic assays for PRO, or for the affinity
CC purification of PRO from recombinant cell culture or natural sources. The
CC present sequence encodes a PRO protein of the invention
XX
SQ Sequence 1218 BP; 292 A; 299 C; 360 G; 267 T; 0 U; 0 Other;

Query Match 100.0%; Score 1218; DB 8; Length 1218;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 AAGGAGTCGCGCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGT 120
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Job time : 534 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 4, 2004, 04:53:16 ; Search time 4802 Seconds
(without alignments)
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1218	100.0	1218	6	AX403653	AX403653 Sequence
2	1218	100.0	1218	6	AX454420	AX454420 Sequence
3	1218	100.0	1218	6	AX490898	AX490898 Sequence
4	1218	100.0	1218	6	AX696937	AX696937 Sequence
5	1218	100.0	1218	9	AY358548	AY358548 Homo sapi
c 6	768	63.1	198253	9	AC009090	AC009090 Homo sapi
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9	668.8	54.9	3586	9	AK027549	AK027549 Homo sapi
10	628.4	51.6	2453	9	AB072745	AB072745 Macaca fa
11	606	49.8	3359	10	BC054121	BC054121 Mus muscu
12	506.8	41.6	3473	9	AB075852	AB075852 Homo sapi
c 13	505.8	41.5	211897	2	AC118500	AC118500 Rattus no
14	505.4	41.5	2084	9	BC013173	BC013173 Homo sapi
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16	497.4	40.8	188704	10	AC123826	AC123826 Mus muscu
17	497.4	40.8	214920	2	AC140182	AC140182 Mus muscu
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20	479	39.3	1937	6	BD249849	BD249849 33 human
21	479	39.3	1937	6	BD131002	BD131002 67 Human
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24	426.2	35.0	618	6	BD147880	BD147880 Primer fo
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26	318.8	26.2	462	6	AR415624	AR415624 Sequence
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28	240.8	19.8	201758	2	AC102358	AC102358 Mus muscu
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36	50	4.1	89944	9	AC093127	AC093127 Papio anu
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ALIGNMENTS

RESULT 1
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LOCUS AX403653 1218 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 8 from Patent WO0077037.
ACCESSION AX403653
VERSION AX403653.1 GI:21437113
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ashkenazi,A., Baker,K., Botstein,D., Desnoyers,L., Eaton,D.L.,
Ferrara,N., Fong,S., Gao,W.Q., Gerber,H., Gerritsen,M.E.,
Goddard,A., Godowski,P., Gurney,A., Kljavin,I.J., Mather,J.,

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          Napier,M., Pan,J., Paoni,N., Roy,M., Tumas,D., Watanabe,C.,
          Williams,P.M., Wood,W.I. and Zhang,Z.
  TITLE   Secreted and transmembrane polypeptides and nucleic acids encoding
          the same
  JOURNAL Patent: WO 0077037-A 8 21-DEC-2000;
          Genentech Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1218
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ORIGIN

  Query Match           100.0%;  Score 1218;  DB 6;  Length 1218;
  Best Local Similarity  100.0%;  Pred. No. 1.3e-289;
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Qy          1 CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACA 60
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Qy         61 AAGGAGTCGCGCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGT 120
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Db       1201 CTATGATCTTTATTAGAG 1218


RESULT 2
AX454420
LOCUS       AX454420                1218 bp    DNA     linear   PAT 06-JUL-2002
DEFINITION  Sequence 5 from Patent WO0208284.
ACCESSION   AX454420
VERSION     AX454420.1  GI:21713834
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE   1
  AUTHORS   Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
            Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
            Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
            and Ye,W.
  TITLE     Compositions and methods for the diagnosis and treatment of
            disorders involving angiogenesis
  JOURNAL   Patent: WO 0208284-A 5 31-JAN-2002;
            Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone
            (US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,
            Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;
            Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US)
            ; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;
            Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William
            I. (US)
FEATURES             Location/Qualifiers
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ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 1.3e-289;
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Qy       421 CTTCTGAGGAGGCTGCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCT 480
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Qy       721 TACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACAC 780
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Qy       961 AGTATCTGACTCACGGTCACCTCCAGTGGAATGAAAAGTGTTCTGCCCGGAACCATGACT 1020
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Qy      1021 TTAGGACTCCTTCAGTTCCTTTAGGACATACTCGCCAAGCCTTGTGCTCACAGGGCAAAG 1080
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Qy      1201 CTATGATCTTTATTAGAG 1218
Db      1201 CTATGATCTTTATTAGAG 1218
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RESULT 3
AX490898
LOCUS AX490898 1218 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 5 from Patent WO0200690.
ACCESSION AX490898
VERSION AX490898.1 GI:22323786
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J., Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I. and Ye,W.
TITLE Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis
JOURNAL Patent: WO 0200690-A 5 03-JAN-2002;
Genentech, Inc. (US)
FEATURES Location/Qualifiers
source 1. .1218
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Query Match 100.0%; Score 1218; DB 6; Length 1218;
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Db        661 TCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTAC 720

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Db       1201 CTATGATCTTTATTAGAG 1218
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DEFINITION  Sequence 5 from Patent WO0078961.
ACCESSION   AX696937
VERSION     AX696937.1  GI:29497951
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ferrara,N., Stewart,T.A., Williams,P.M., Baker,K.P., Desnoyers,L.,
            Eaton,D.L., Gao,W.Q., Pan,J., Botstein,D., Fong,S., Goddard,A.,
            Godowski,P.J., Gurney,A.L., Smith,V., Tumas,D., Wood,W.I.,
            Grimaldi,C.J., Hillan,K.J., Paoni,N.F., Roy,M.A. and Watanabe,C.K.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
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  JOURNAL   Patent: WO 0078961-A 5 28-DEC-2000;
            Genentech Inc. (US)
FEATURES             Location/Qualifiers
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DEFINITION  Homo sapiens clone DNA26846 IVFG328 (UNQ328) mRNA, complete cds.
ACCESSION   AY358548
VERSION     AY358548.1  GI:37182218
KEYWORDS    FLI_CDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1218)
  AUTHORS   Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
            Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
            Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
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            Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
            Goddard,A., Wood,W.I. and Godowski,P.
  TITLE     The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
            Effort to Identify Novel Human Secreted and Transmembrane Proteins:
            A Bioinformatics Assessment
  JOURNAL   Genome Res. 13 (10), 2265-2270 (2003)
   PUBMED   12975309
REFERENCE   2  (bases 1 to 1218)
  AUTHORS   Clark,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
            Inc., 1 DNA Way, South San Francisco, CA 94080, USA
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ORIGIN

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Qy        181 GAGGGTTGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACC 240
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Qy        841 GGACCCTGTTCGGCCACCAAGGAGGGGCCGAGGACCTCATGAGCCAAGGAGAAAGAAACA 900
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RESULT 6
AC009090/c
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DEFINITION  Homo sapiens chromosome 16 clone RP11-407G23, complete sequence.
ACCESSION   AC009090
VERSION     AC009090.12  GI:29124043
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 198253)
  AUTHORS   DOE Joint Genome Institute, Stanford Human Genome Center and Los
            Alamos National Laboratory.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 198253)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE   3  (bases 1 to 198253)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-APR-2002) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE   4  (bases 1 to 198253)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-DEC-2002) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE   5  (bases 1 to 198253)
  AUTHORS   DOE Joint Genome Institute, Stanford Human Genome Center and Los
            Alamos National Laboratory.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell
            Drive, Walnut Creek, CA 94598, USA
COMMENT     On Mar 19, 2003 this sequence version replaced gi:27151360.
            Draft Sequence Produced by DOE Joint Genome Institute
            www.jgi.doe.gov
            Finishing Completed at Stanford Human Genome Center and Los Alamos
            National Laboratory
            www-shgc.stanford.edu
            Quality: Phrap Quality >=40 100% of Sequence;
            Estimated Total Number of Errors is 0.
            NOTE: BACTERIAL TRANSPOSON  excised at 62920.
FEATURES             Location/Qualifiers
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                     /clone="RP11-407G23"
ORIGIN

  Query Match             63.1%;  Score 768;  DB 9;  Length 198253;
  Best Local Similarity   100.0%;  Pred. No. 2e-178;
  Matches  768;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        451 AGAACTGCCATTGGATGTCCAGAATCCCCTGTAGTTGATAATGTTGGGAATAAGCTCTGC 510
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Db      59076 AGAACTGCCATTGGATGTCCAGAATCCCCTGTAGTTGATAATGTTGGGAATAAGCTCTGC 59017

Qy        511 AACTTTCTTTGGCATTCAGTTGTTAAAAACAAATAGGATGCAAATTCCTCAACTCCAGGT 570
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      59016 AACTTTCTTTGGCATTCAGTTGTTAAAAACAAATAGGATGCAAATTCCTCAACTCCAGGT 58957

Qy        571 TATGAAAACAGTACTTGGAAAACTGAAAACTACCTAAATGATCGTCTTTGGTTGGGCCGT 630
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Db      58956 TATGAAAACAGTACTTGGAAAACTGAAAACTACCTAAATGATCGTCTTTGGTTGGGCCGT 58897

Qy        631 GTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAGCACATAGC 690
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Qy        751 TGACAGTGGAACAGATGACAGTGTTGACACCCAACAGCAACAGGCCGAGAACAGTGCAGT 810
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Db      58776 TGACAGTGGAACAGATGACAGTGTTGACACCCAACAGCAACAGGCCGAGAACAGTGCAGT 58717

Qy        811 ACCCACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTCGGCCACCAAGGAGGGGCCG 870
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Db      58716 ACCCACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTCGGCCACCAAGGAGGGGCCG 58657

Qy        871 AGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTTGGACACACT 930
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Db      58656 AGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTTGGACACACT 58597

Qy        931 GGCAGTAATACGGACTCTTGTAGATAAGTAAGTATCTGACTCACGGTCACCTCCAGTGGA 990
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Db      58596 GGCAGTAATACGGACTCTTGTAGATAAGTAAGTATCTGACTCACGGTCACCTCCAGTGGA 58537

Qy        991 ATGAAAAGTGTTCTGCCCGGAACCATGACTTTAGGACTCCTTCAGTTCCTTTAGGACATA 1050
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Qy       1051 CTCGCCAAGCCTTGTGCTCACAGGGCAAAGGAGAATATTTTAATGCTCCGCTGATGGCAG 1110
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Db      58476 CTCGCCAAGCCTTGTGCTCACAGGGCAAAGGAGAATATTTTAATGCTCCGCTGATGGCAG 58417

Qy       1111 AGTAAATGATAAGATTTGATGTTTTTGCTTGCTGTCATCTACTTTGTCTGGAAATGTCTA 1170
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Db      58416 AGTAAATGATAAGATTTGATGTTTTTGCTTGCTGTCATCTACTTTGTCTGGAAATGTCTA 58357

Qy       1171 AATGTTTCTGTAGCAGAAAACACGATAAAGCTATGATCTTTATTAGAG 1218
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Db      58356 AATGTTTCTGTAGCAGAAAACACGATAAAGCTATGATCTTTATTAGAG 58309


RESULT 7
AX879845
LOCUS       AX879845               3586 bp    DNA     linear   PAT 17-DEC-2003
DEFINITION  Sequence 14750 from Patent EP1074617.
ACCESSION   AX879845
VERSION     AX879845.1  GI:40034581
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
            Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
  TITLE     Primers for synthesising full-length cDNA and their use
  JOURNAL   Patent: EP 1074617-A 14750 07-FEB-2001;
            Research Association for Biotechnology (JP)
FEATURES             Location/Qualifiers
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                     SRIRQISHIS"
ORIGIN

  Query Match           54.9%;  Score 668.8;  DB 6;  Length 3586;
  Best Local Similarity  78.0%;  Pred. No. 4.8e-154;
  Matches  945;  Conservative    0;  Mismatches    2;  Indels  265;  Gaps    1;

Qy         11 CGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACAAAGGAGTCGC 70
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Db         12 CAGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACAAAGGAGTCGC 71

Qy         71 GCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGTCAGTGCCACA 130
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Db         72 GCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGTCAGTGCCACA 131

Qy        131 GCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGGTTGGG 190
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Db        132 GCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGGTTGGG 191

Qy        191 GACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGACTGGGGC 250
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Qy        251 CGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACA 310
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Db        252 CGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACA 311

Qy        311 GCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCCTAGAAGAGG 370
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Db        312 GCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCCTAGAAGAGG 371

Qy        371 GTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCCCTTCTGAGGA 430
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Db        432 GGCTGCGGCTAACAGGGCCCAGGTGAGAGGCAGCTATCTATCTCCTGGGGTGGCTCCTGG 491

Qy        452 ------------------------------------------------------------ 451

Db        492 TACCGATGGAGTCCTGACCTACTCAGGGGTGCCCGGGATAGAAAGGGTAGATGAAGGGAC 551

Qy        452 ------------------------------------------------------------ 451

Db        552 GCTTTAGGAGGGTTCTTTTTGTGGAGTTTACGGTCTAGGTGGCACGGATGAGGCATACCT 611

Qy        452 ------------------------------------------------------------ 451

Db        612 CCCCGAGGAGATTTAGAAACGCCTTGGGATAGAAAGAGAATGGGGCTAGGAAGCAGGAGC 671

Qy        452 ----------------------------------------------GAACTGCCATTGGA 465
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Db        672 TAGAACTAGCGGAATGTCCTACTACGGAAGCCGGAGCTGAAAATTGGAACTGCCATTGGA 731

Qy        466 TGTCCAGAATCCCCTGTAGTTGATAATGTTGGGAATAAGCTCTGCAACTTTCTTTGGCAT 525
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Db        732 TGTCCAGAATCCCCTGTAGTTGATAATGTTGGGAATAAGCTCTGCAACTTTCTTTGGCAT 791

Qy        526 TCAGTTGTTAAAAACAAATAGGATGCAAATTCCTCAACTCCAGGTTATGAAAACAGTACT 585
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Db        792 TCAGTTGTTAAAAACAAATAGGATGCAAATTCCTCAACTCCAGGTTATGAAAACAGTACT 851

Qy        586 TGGAAAACTGAAAACTACCTAAATGATCGTCTTTGGTTGGGCCGTGTTCTTAGCGAGCAG 645
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Db        852 TGGAAAACTGAAAACTACCTAAATGATCGTCTTTGGTTGGGCCGTGTTCTTAGCGAGCAG 911

Qy        646 AAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGAC 705
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Db        912 AAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGAC 971

Qy        706 TGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGA 765
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Db        972 TGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGA 1031

Qy        766 TGACAGTGTTGACACCCAACAGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACAC 825
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Db       1032 TGACAGTGTTGACACCCAACAGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACAC 1091

Qy        826 AAGGAGCCAACCACGGGACCCTGTTCGGCCACCAAGGAGGGGCCGAGGACCTCATGAGCC 885
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Db       1092 AAGGAGCCAACCACGGGACCCTGTTCGGCCACCAAGGAGGGGCCGAGGACCTCATGAGCC 1151

Qy        886 AAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTTGGACACACTGGCAGTAATACGGAC 945
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Db       1152 AAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTTGGACACACTGGCAGTAATACGGAC 1211

Qy        946 TCTTGTAGATAA 957
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RESULT 8
BD158056
LOCUS       BD158056                3586 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Primer for synthesizing full-length cDNA and use thereof.
ACCESSION   BD158056
VERSION     BD158056.1  GI:27863814
KEYWORDS    JP 2002191363-A/12899.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3586)
  AUTHORS   Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
            Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
  TITLE     Primer for synthesizing full-length cDNA and use thereof
  JOURNAL   Patent: JP 2002191363-A 12899 09-JUL-2002;
            HELIX RESEARCH INSTITUTE
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002191363-A/12899
            PD   09-JUL-2002
            PF   28-JUL-2000 JP 2000280990
            PI   TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU
            PI   SAITO,
            PI   JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
            PI   KEIICHI NAGAI,TETSUJI OTSUKI
            PC
            C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
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             Primer for synthesizing full-length cDNA and use thereof FH   Key
                     Location/Qualifiers
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FEATURES                Location/Qualifiers
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ORIGIN
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  Query Match             54.9%;  Score 668.8;  DB 6;  Length 3586;
  Best Local Similarity   78.0%;  Pred. No. 4.8e-154;
  Matches  945;  Conservative    0;  Mismatches    2;  Indels  265;  Gaps    1;

Qy         11 CGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACAAAGGAGTCGC 70
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Qy         71 GCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGTCAGTGCCACA 130
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Qy        452 ------------------------------------------------------------ 451

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Qy        452 ------------------------------------------------------------ 451

Db        612 CCCCGAGGAGATTTAGAAACGCCTTGGGATAGAAAGAGAATGGGGCTAGGAAGCAGGAGC 671

Qy        452 ----------------------------------------------GAACTGCCATTGGA 465
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Db        672 TAGAACTAGCGGAATGTCCTACTACGGAAGCCGGAGCTGAAAATTGGAACTGCCATTGGA 731

Qy        466 TGTCCAGAATCCCCTGTAGTTGATAATGTTGGGAATAAGCTCTGCAACTTTCTTTGGCAT 525
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Qy        586 TGGAAAACTGAAAACTACCTAAATGATCGTCTTTGGTTGGGCCGTGTTCTTAGCGAGCAG 645
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Qy        646 AAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGAC 705
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Db        912 AAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGAC 971

Qy        706 TGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGA 765
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Db        972 TGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGA 1031

Qy        766 TGACAGTGTTGACACCCAACAGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACAC 825
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Qy        886 AAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTTGGACACACTGGCAGTAATACGGAC 945
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Db       1152 AAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTTGGACACACTGGCAGTAATACGGAC 1211

Qy        946 TCTTGTAGATAA 957
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Db       1212 TCTTGTAGATAA 1223


RESULT 9
AK027549
LOCUS       AK027549               3586 bp    mRNA    linear   PRI 01-AUG-2002
DEFINITION  Homo sapiens cDNA FLJ14643 fis, clone NT2RP2001597, weakly similar
            to RYANODINE RECEPTOR, CARDIAC MUSCLE.
ACCESSION   AK027549
VERSION     AK027549.1  GI:14042305
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
            Nishikawa,T., Nagai,K., Sugano,S., Takahashi-Fujii,A., Hara,H.,
            Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R., Takeuchi,K.,
            Arita,M., Nabekura,T., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J.,
            Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuho,Y. and Oshima,A.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 3586)
  AUTHORS   Isogai,T. and Otsuki,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute,
            Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology; cDNA library construction,
            5'- & 3'-end one pass sequencing and clone selection: Helix
            Research Institute (supported by Japan Key Technology Center etc.)
            and Department of Virology, Institute of Medical Science,
            University of Tokyo.
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             54.9%;  Score 668.8;  DB 9;  Length 3586;
  Best Local Similarity   78.0%;  Pred. No. 4.8e-154;
  Matches  945;  Conservative    0;  Mismatches    2;  Indels  265;  Gaps    1;

Qy         11 CGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACAAAGGAGTCGC 70
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Db         12 CAGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACAAAGGAGTCGC 71

Qy         71 GCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGTCAGTGCCACA 130
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Qy       191 GACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGACTGGGGC 250
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Qy       251 CGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACA 310
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Qy       311 GCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCCTAGAAGAGG 370
Db       312 GCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCCTAGAAGAGG 371
Qy       371 GTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCCCTTCTGAGGA 430
Db       372 GTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTCCTTGGGGGTCGCCCTTCTGAGGA 431
Qy       431 GGCTGCGGCTAACAGGGCCCA---------------------------------------- 451
Db       432 GGCTGCGGCTAACAGGGCCCAGGTGAGAGGCAGCTATCTATCTCCTGGGGTGGCTCCTGG 491
Qy       452 ---------------------------------------------------------- 451
Db       492 TACCGATGGAGTCCTGACCTACTCAGGGGTGCCCGGGATAGAAAGGGTAGATGAAGGGAC 551
Qy       452 ---------------------------------------------------------- 451
Db       552 GCTTTAGGAGGGTTCTTTTTGTGGAGTTTACGGTCTAGGTGGCACGGATGAGGCATACCT 611
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Qy       452 ----------------------------------------------GAACTGCCATTGGA 465
Db       672 TAGAACTAGCGGAATGTCCTACTACGGAAGCCGGAGCTGAAAATTGGAACTGCCATTGGA 731
Qy       466 TGTCCAGAATCCCCTGTAGTTGATAATGTTGGGAATAAGCTCTGCAACTTTCTTTGGCAT 525
Db       732 TGTCCAGAATCCCCTGTAGTTGATAATGTTGGGAATAAGCTCTGCAACTTTCTTTGGCAT 791
Qy       526 TCAGTTGTTAAAAACAAATAGGATGCAAATTCCTCAACTCCAGGTTATGAAAACAGTACT 585
Db       792 TCAGTTGTTAAAAACAAATAGGATGCAAATTCCTCAACTCCAGGTTATGAAAACAGTACT 851
Qy       586 TGGAAAACTGAAAACTACCTAAATGATCGTCTTTGGTTGGGCCGTGTTCTTAGCGAGCAG 645
Db       852 TGGAAAACTGAAAACTACCTAAATGATCGTCTTTGGTTGGGCCGTGTTCTTAGCGAGCAG 911
Qy       646 AAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGAC 705
Db       912 AAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGAC 971
Qy       706 TGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGA 765
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Qy       946 TCTTGTAGATAA 957
Db      1212 TCTTGTAGATAA 1223
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RESULT 10
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LOCUS       AB072745               2453 bp    mRNA    linear   PRI 22-FEB-2003
DEFINITION  Macaca fascicularis testis cDNA clone:QtsA-15931, full insert
            sequence.
ACCESSION   AB072745
VERSION     AB072745.1  GI:16041093
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Macaca fascicularis (crab-eating macaque)
  ORGANISM  Macaca fascicularis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
            Cercopithecinae; Macaca.
REFERENCE   1
  AUTHORS   Osada,N., Hida,M., Kusuda,J., Tanuma,R., Hirata,M., Suto,Y.,
            Hirai,M., Terao,K., Sugano,S. and Hashimoto,K.
  TITLE     Cynomolgus monkey testicular cDNAs for discovery of novel human
            genes in the human genome sequence
  JOURNAL   BMC Genomics 3 (1), 36 (2002)
   PUBMED   12498619
REFERENCE   2  (bases 1 to 2453)
  AUTHORS   Hashimoto,K., Osada,N., Hida,M., Kusuda,J. and Sugano,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-OCT-2001) Katsuyuki Hashimoto, National Institute of
            Infectious Diseases, Division of Genetic Resources; 23-1, Toyama
            1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
            (E-mail:khashi@nih.go.jp, URL:http://www.nih.go.jp/yoken/genebank/,
            Tel:81-3-5285-1111(ex.2120), Fax:81-3-5285-1181)
COMMENT     Lab host:    TOP10
            Vector:      pME18S-FL3 (Acc.No. AB009864)
            R. Site1:    DraIII (CACTGTGTG)
            R. Site2:    DraIII (CACCATGTG)
            Description: 1st strand cDNA was primed with an oligo(dT) primer
            [ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was synthesized
            using specific 5' and 3' primers and amplified by PCR.  The PCR
            product was digested with SfiI and size selection was performed to
            exclude fragments <1.5kb.The SfiI-digested PCR product was cloned
            into distinct DraIII sites of pME18S-FL3. XhoI sites just outside
            the DraIII sites can be used to isolate the cDNA insert.  Libraries
            were constructed by oligo-capping method
            (Sugano et al.,University of Tokyo, Institute of Medical Science).
            Custom primer used for sequencing
            ( 5' end primer [CTTCTGCTCTAAAAGCTGCG];
            3' end primer [CGACCTGCAGCTCGAGCACA] ).
FEATURES             Location/Qualifiers
     source          1. .2453
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                     /clone="QtsA-15931"
                     /sex="male"
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SRIRQISHIS"

ORIGIN

Query Match 51.6%; Score 628.4; DB 9; Length 2453;
Best Local Similarity 83.9%; Pred. No. 4.4e-144;
Matches 799; Conservative 0; Mismatches 31; Indels 122; Gaps 3;

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Qy         11 CGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACAAAGGAGTCGC 70
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Db         61 CAGCGCCGTGGCCTCGCGTCCATCTTTACCGTTCTCTCGGACCTGTCACAAAGGAGTCGC 120

Qy         71 GCCGCCGCCGCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGTCAGTGCCACA 130
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Db        121 GCCGCCGC------CCCCTCGCTCCGGTGGGCCCGGGAGCTAGAGAAAGTCAGTGCTGCA 174

Qy        131 GCCCGACCGCGCTGCTCTGAG-----CCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGG 185
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Db        175 GCCCGACCGCGCTGCTCTGAGAAGCCCCCTGGGCACGCGGAGCGGGAGGGAGTGTGAGGG 234

Qy        186 TTGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGACT 245
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Db        235 TTGGAGGCGACTGTGAGGGAG---------------------------------------- 255

Qy        246 GGGGCCGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAACCTGAG 305

Db        256 ------------------------------------------------------------ 255

Qy        306 AAACAGCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCCTAGA 365
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Db        256 -----------GGTTTTCCACCGAGGCCCGCGCTTGAGGAATCCGAAGAGGTTCCTAGA 303

Qy        366 AGAGGGTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCCCTTCT 425
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Db        304 AGAGGGTGTTCCCTCTTTCGGGGGTCCTCACCAGAAGAGGTTCTTGGGGGTCGCCCTTCT 363

Qy        426 GAGGAGGCTGCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCTGTAGT 485
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Qy        486 TGATAATGTTGGGAATAAGCTCTGCAACTTTCTTTGGCATTCAGTTGTTAAAAACAAATA 545
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Qy        606 AAATGATCGTCTTTGGTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGT 665
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Db        544 AAATGATCGTCCTTGGTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGC 603

Qy        666 TGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTACTACCA 725
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Db        604 TGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGAACTAGAGGTGCCACTACTACCA 663

Qy        726 TGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACACCCAAC 785
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Db        664 TGGGTAATTCCTGTATCTGCCGAGATGACAGTGGGACAGATGACAGTGTCGACACCCAGC 723

Qy        786 AGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACACAAGGAGCCAACCACGGGACC 845
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Db        724 AGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACACAAGGAGCCAACCACGGGACC 783

Qy        846 CTGTTCGGCCACCAAGGAGGGGCCGAGGACCTCATGAGCCAAGGAGAAAGAAACAAAATG 905
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Db        784 CTGTTCGGCCTCCGAGGAGGGGCCGAGGACCACATGAGCCAAGGAGAAAGAAACAAAATG 843

Qy        906 TGGATGGGCTAGTGTTGGACACACTGGCAGTAATACGGACTCTTGTAGATAA 957
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RESULT 11
BC054121
LOCUS BC054121 3359 bp mRNA linear ROD 07-OCT-2003
DEFINITION Mus musculus RIKEN cDNA 4930470D19 gene, mRNA (cDNA clone MGC:59548 IMAGE:6393910), complete cds.
ACCESSION BC054121
VERSION BC054121.1 GI:32484165
KEYWORDS MGC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 3359)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE 22388257
PUBMED 12477932
REFERENCE 2 (bases 1 to 3359)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (30-JUN-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freeman, Ph.D.
cDNA Library Preparation: ResGen, Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 109 Row: g Column: 12
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.
FEATURES Location/Qualifiers
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/mol_type="mRNA"

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ORIGIN

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  Best Local Similarity  80.5%;  Pred. No. 1.5e-138;
  Matches  766;  Conservative    0;  Mismatches  165;  Indels   21;  Gaps    4;

Qy         11 CGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACAAAGGAGTCGC 70
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Db         43 CAGTGCCGTGTCCCCGCGTCCATCTTTACCGCTCTCTTGGACCTGTCACAAAGGAGTCGC 102

Qy         71 GCCGCCGCCGCCCGCCCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGTCAGTGCCACA 130
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Db        103 GCCGCTGTCGCTGTCCCCTCCCTCCGGTGGGCCCAGGAGCTAGTGCAAGTCAGTGCCACA 162

Qy        131 GCCCGACCGCGCTGCTCTGAG-----CCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGG 185
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Db        163 GCCCGACCGCGCTGCTCTGGGAAGCCCCTTGGGGACGTGGCCGGGGAGGGAGCTTGAGGG 222

Qy        186 TTGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGACT 245
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Qy        546 GGATGCAAATTCCTCAACTCCAGGTTATGAAAACAGTACTTGGAAAACTGAAAACTACCT 605
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Qy        606 AAATGATCGTCTTTGGTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGT 665
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Qy        666 TGTTGACTCTCGAAGAGCACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTACTACCA 725
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Qy        726 TGGGTAATTCCTGTATCTGCCGAGATGACAGTGGAACAGATGACAGTGTTGACACCCAAC 785
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Db        747 TGGGTAATTCCTGCATCTGCCGAGATGACAGTGGAGCAGAAGACAATGTTGACACCCACC 806

Qy        786 AGCAACAGGCCGAGAACAGTGCAGTACCCACTGCTGACACAAGGAGCCAACCACGGGACC 845
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Qy        846 CTGTTCGGCCACCAAGGAGGGGCCGAGGACCTCATGAGCCAAGGAGAAAGAAACAAAATG 905
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Qy        906 TGGATGGGCTAGTGTTGGACACACTGGCAGTAATACGGACTCTTGTAGATAA 957
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Db        927 TGGATGGGTTAGTGCTGGACACACTGGCGGTAATACGGACTCTTGTAGATAA 978


RESULT 12
AB075852
LOCUS       AB075852               3473 bp    mRNA    linear   PRI 26-FEB-2002
DEFINITION  Homo sapiens mRNA for KIAA1972 protein.
ACCESSION   AB075852
VERSION     AB075852.1  GI:18916844
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Nagase,T., Kikuno,R. and Ohara,O.
  TITLE     Prediction of the coding sequences of unidentified human genes.
            XXII. The complete sequences of 50 new cDNA clones which code for
            large proteins
  JOURNAL   DNA Res. 8 (6), 319-327 (2001)
  MEDLINE   21842142
   PUBMED   11853319
REFERENCE   2  (bases 1 to 3473)
  AUTHORS   Ohara,O., Nagase,T. and Kikuno,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-DEC-2001) Osamu Ohara, Kazusa DNA Research Institute,
            Department of Human Gene Research; 1532-3, Yana, Kisarazu, Chiba
            292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp,
            URL:http://www.kazusa.or.jp/huge, Tel:81-438-52-3913,
            Fax:81-438-52-3914)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="fk09334"
                     /tissue_type="brain"
                     /note="vector:pBluescriptII SK plus"
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                     /gene="KIAA1972"
     CDS             <244. .1974
                     /gene="KIAA1972"
                     /note="start codon is not identified."
                     /codon_start=1
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/evidence=not_experimental
/product="KIAA1972 protein"
/protein_id="BAB85558.1"
/db_xref="GI:18916845"
/translation="MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSC
ICRDDSGTDDSVDTQQQQAENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDG
LVLDTLAVIRTLVDNDQEPPYSMITLHEMAETDEGWLDVVQSLIRVIPLEDPLGPAVI
TLLLDECPLPTKDALQKLTEILNLNGEVACQDSSHPAKHRNTSAVLGCLAEKLAGPAS
IGLLSPGILEYLLQCLKLQSHPTVMLFALIALEKFAQTSENKLTISESSISDRLVTLE
SWANDPDYLKRQVGFCAQWSLDNLFLKEGRQLTYEKVNLSSIRAMLNSNDVSEYLKIS
PHGLEARCDASSFESVRCTFCVDAGVWYYEVTVVTSGVMQIGWATRDSKFLNHEGYGI
GDDEYSCAYDGCRQLIWYNARSKPHIHPCWKEGDTVGFLLDLNEKQMIFFLNGNQLPP
EKQVFSSTVSGFFAAASFMSYQQCEFNFGAKPFKYPPSMKFSTFNDYAFLTAEEKIIL
PRHRRLALLKQVSIRENCCSLCCDEVADTQLKPCGHSDLCMDCALQLETCPLCRKEIV
SRIRQISHIS"

ORIGIN

Query Match 41.6%; Score 506.8; DB 9; Length 3473;
Best Local Similarity 99.6%; Pred. No. 4.6e-114;
Matches 508; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy        448 CCCAGAACTGCCATTGGATGTCCAGAATCCCCTGTAGTTGATAATGTTGGGAATAAGCTC 507
              | | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 CTCCGAACTGCCATTGGATGTCCAGAATCCCCTGTAGTTGATAATGTTGGGAATAAGCTC 143

Qy        508 TGCAACTTTCTTTGGCATTCAGTTGTTAAAAACAAATAGGATGCAAATTCCTCAACTCCA 567
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 TGCAACTTTCTTTGGCATTCAGTTGTTAAAAACAAATAGGATGCAAATTCCTCAACTCCA 203

Qy        568 GGTTATGAAAACAGTACTTGGAAAACTGAAAACTACCTAAATGATCGTCTTTGGTTGGGC 627
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Db        204 GGTTATGAAAACAGTACTTGGAAAACTGAAAACTACCTAAATGATCGTCTTTGGTTGGGC 263

Qy        628 CGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAGCACAT 687
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 CGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAGCACAT 323

Qy        688 AGCCCACTTCCTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTGCCG 747
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 AGCCCACTTCCTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTGCCG 383

Qy        748 AGATGACAGTGGAACAGATGACAGTGTTGACACCCAACAGCAACAGGCCGAGAACAGTGC 807
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Db        384 AGATGACAGTGGAACAGATGACAGTGTTGACACCCAACAGCAACAGGCCGAGAACAGTGC 443

Qy        808 AGTACCCACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTCGGCCACCAAGGAGGGG 867
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Db        444 AGTACCCACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTCGGCCACCAAGGAGGGG 503

Qy        868 CCGAGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTTGGACAC 927
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CCGAGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTTGGACAC 563

Qy        928 ACTGGCAGTAATACGGACTCTTGTAGATAA 957
              |||||||||||||||||||||||||||||
Db        564 ACTGGCAGTAATACGGACTCTTGTAGATAA 593
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RESULT 13
AC118500/c
LOCUS AC118500 211897 bp DNA linear HTG 19-NOV-2002
DEFINITION Rattus norvegicus clone CH230-144P21, WORKING DRAFT SEQUENCE, 6 unordered pieces.
ACCESSION AC118500
VERSION AC118500.4 GI:25073691
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 211897)
AUTHORS Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D., Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M., Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A., Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwackelemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C., Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L., Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 211897)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (18-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE 3 (bases 1 to 211897)
AUTHORS Rat Genome Sequencing Consortium.
TITLE Direct Submission
JOURNAL Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
COMMENT On Nov 19, 2002 this sequence version replaced gi:23269807.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome

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          shotgun sequence only contigs will be indicated in the feature
          table.
          -------------- Genome Center
              Center: Baylor College of Medicine
              Center code: BCM
              Web site: http://www.hgsc.bcm.tmc.edu/
              Contact: hgsc-help@bcm.tmc.edu
          -------------- Project Information
              Center project name: GUIK
              Center clone name: CH230-144P21
          -------------- Summary Statistics
              Assembly program: Phrap; version 0.990329
              Consensus quality: 199093 bases at least Q40
              Consensus quality: 201840 bases at least Q30
              Consensus quality: 203801 bases at least Q20
              Estimated insert size: 205170; sum-of-contigs estimation
              Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
          --------------
          * NOTE: Estimated insert size may differ from sequence length
          *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
          * NOTE: This is a 'working draft' sequence. It currently
          * consists of 6 contigs. The true order of the pieces
          * is not known and their order in this sequence record is
          * arbitrary. Gaps between the contigs are represented as
          * runs of N, but the exact sizes of the gaps are unknown.
          * This record will be updated with the finished sequence
          * as soon as it is available and the accession number will
          * be preserved.
          *       1   158307: contig of 158307 bp in length
          *  158308   158407: gap of unknown length
          *  158408   178882: contig of 20475 bp in length
          *  178883   178982: gap of unknown length
          *  178983   198357: contig of 19375 bp in length
          *  198358   198457: gap of unknown length
          *  198458   209332: contig of 10875 bp in length
          *  209333   209432: gap of unknown length
          *  209433   210436: contig of 1004 bp in length
          *  210437   210536: gap of unknown length
          *  210537   211897: contig of 1361 bp in length.
FEATURES             Location/Qualifiers
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                     /organism="Rattus norvegicus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10116"
                     /clone="CH230-144P21"
     misc_feature    1. .1700
                     /note="wgs_contig"
     misc_feature    183448. .184725
                     /note="wgs_contig"
ORIGIN

  Query Match             41.5%;  Score 505.8;  DB 2;  Length 211897;
  Best Local Similarity   83.8%;  Pred. No. 1e-113;
  Matches  621;  Conservative    0;  Mismatches  112;  Indels    8;  Gaps    4;

Qy        450 CAGAACTGCCATTGGATGTCCAGAATCCCCTGTAGTTGATAATGTTGGGAATAAGCTCTG 509
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Db      99551 CAGAGCTGCCAGTGTATGGCCAGCATTCCCAGTGGTTAATAATGTTGGAAACGAGCTGCT 99492

Qy        510 CAACTTTCTTTGGCATTCAGTTGTTAAAAACAAATAGGATGCAAATTCCTCAACTCCAGG 569
                || ||||   || |||||||||||| ||  |||||  ||||| |   |||||||||
Db      99491 TGACCTTCTCCAGCCTTCAGTTGTTAAGAATGAATAGAGTGCAAGT---TCAACTCCACA 99435

Qy        570 TTATGAAAACAGTACTTGGAAAACTGAAAACTACCTAAATGATCGTCTTTGGTTGGGCCG 629
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Db      99434 TTATGAAGACAGTACTCGGAAAATTGAAAACTATCTAAATGATTGTCTTTGGTTGGGCTG 99375

Qy        630 TGTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAGCACATAG 689
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Db      99374 TGTTCTTAGCAAGCAGAAGCCTTGGTCAGGGTCTGCTATTGACTCTTGAGGAGCACATAG 99315

Qy        690 CCCACTTCCTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTGCCGAG 749
              ||||| |  | ||||||  ||||||| ||||||| |||||||||| || ||||||||||

Db      99314 CCCACCTATTGGGGACTACAGGTGCCACTACTACTATGGGTAATTCTTGCATCTGCCGAG 99255

Qy        750 ATGACAGTGGAACAGATGACAGTGTTGACACCCAACAGCAACAGGCCGAGAACAGTGCAG 809
              |||||||||| |||| |||||||||||||||| |||||||||| |||||||| |||
Db      99254 ATGACAGTGGAGCAGAAGACAGTGTTGACACCCACCAGCAACAGGCTGAGAACAGTACAG 99195

Qy        810 TACCCACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTCGGCCACCAAGGAGGGGCC 869
              | || ||||| |||| |||||||||| |||||||||||||||||| |||||||| ||||
Db      99194 TCCCTACTGCGGACAGTAGGAGCCAACTTCGGGACCCTGTTCGGCCTCCAAGGAGAGGCC 99135

Qy        870 GAGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTTGGACACAC 929
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db      99134 GAGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGTTAGTGTTGGACACAC 99075

Qy        930 TGGCAGTAATACGGACTCTTGTAGATAAGTAAGTATCTGACTCACGGTCACCTCCAGTGG 989
              |||| |||||||||||||||||||||||||||||||||||||||| ||  || |||||||||
Db      99074 TGGCGGTAATACGGACTCTTGTAGATAAGTAAGTATCTGACTTACTATCGCCTCCAGTGT 99015

Qy        990 AATGAAAAGTGTTCTGCCCGGAACCATGACTTTAGGACTCCTTCAGTTCCTTTAGGACAT 1049
              ||| ||||||| ||||| ||||||| ||||| |||||||||| ||  ||||||| ||
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Qy       1050 ACTCGCCAAGCCTTGTGCTCACAGGGCAAAGGAGAATATTTTAATGCTCCGCTGATGGCA 1109
              | |  | |||||||||||| | ||| ||| |||||||  ||| | |||| |||||||||
Db      98954 ATTTTCTAAGCCTTGTGCTAATAGGCCAAGAGAGAATA-CTTATTTCTCCTCTGATGGCA 98896

Qy       1110 GAGTAAATGATAAGATTTGATGTTTTTGCTTGCTGTCATCTACT-TTGTCTGGAAATGTC 1168
              ||||||  | ||| |||||||||||| |||||| |||||||||  |||||||||| ||
Db      98895 GAGTAA---ACAAGGTTTGATGTTTTTACTTGCTATCATCTACTCCTGTCTGGAAAGGTT 98839

Qy       1169 TAAATGTTTCTGTAGCAGAAA 1189
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Db      98838 TGAACATTTCTGTACAGAAAA 98818
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```
RESULT 14
BC013173
LOCUS       BC013173                2084 bp    mRNA    linear   PRI 04-OCT-2003
DEFINITION  Homo sapiens KIAA1972 protein, mRNA (cDNA clone MGC:17340
            IMAGE:4340287), complete cds.
ACCESSION   BC013173
VERSION     BC013173.2  GI:34783185
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2084)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  MEDLINE   22388257
   PUBMED   12477932
REFERENCE   2  (bases 1 to 2084)
  AUTHORS   Strausberg,R.
```

```
  TITLE     Direct Submission
  JOURNAL   Submitted (27-AUG-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     On Sep 16, 2003 this sequence version replaced gi:15341959.
            Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lou Staudt
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Baylor College of Medicine Human Genome
            Sequencing Center
            Center code: BCM-HGSC
            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
            Contact: amg@bcm.tmc.edu
            Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
            Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
            A.N., Gibbs, R.A.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 26 Row: i Column: 4
            This clone was selected for full length sequencing because it
            passed the following selection criteria: Hexamer frequency ORF
            analysis, GenomeScan gene prediction.
FEATURES              Location/Qualifiers
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                      /clone_lib="NIH_MGC_85"
                      /lab_host="DH10B"
                      /note="Vector: pCMV-SPORT6"
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                      LVLDTLAVIRTLVDNDQEPPYSMITLHEMAETDEGWLDVVQSLIRVIPLEDPLGPAVI
                      TLLLDECPLPTKDALQKLTEILNLNGEVACQDSSHPAKHRNTSAVLGCLAEKLAGPAS
                      IGLLSPGILEYLLQCLKLQSHPTVMLFALIALEKFAQTSENKLTISESSISDRLVTLE
                      SWANDPDYLKRQVGFCAQWSLDNLFLKEGRQLTYEKVNLSSIRAMLNSNDVSEYLKIS
                      PHGLEARCDASSFESVRCTFCVDAGVWYYEVTVVTSGVMQIGWATRDSKFLNHEGYGI
                      GDDEYSCAYDGCRQLIWYNARSKPHIHPCWKEGDTVGFLLDLNEKQMIFFLNGNQLPP
                      EKQVFSSTVSGFFAAASFMSYQQCEFNFGAKPFKYPPSMKFSTFNDYAFLTAEEKIIL
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                      SRIRQISHIS"
     misc_feature     1353. .1724
                      /note="SPRY; Region: Domain in SPla and the RYanodine
                      Receptor."
                      /db_xref="CDD:smart00449"
ORIGIN

  Query Match             41.5%;  Score 505.4;  DB 9;  Length 2084;
  Best Local Similarity   99.8%;  Pred. No. 1e-113;
  Matches  506;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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RESULT 15
BD249821
LOCUS       BD249821               2133 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  33 human secreted proteins.
ACCESSION   BD249821
VERSION     BD249821.1  GI:33059591
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  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2133)
  AUTHORS   Rosen,C.A., Ruben,S.M., Ebner,R., Young,P.E., Ni,J., Soppet,D.R.,
            Moore,P.A., Shi,Y., Lafleur,D.W., Olsen,H.S., Florence,K.A. and
            Komatsoulis,G.
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  JOURNAL   Patent: JP 2002540763-A 23 03-DEC-2002;
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            PI   CRAIG A ROSEN,STEVEN M RUBEN,REINHARD EBNER,PAUL E YOUNG,JIAN
            PI   NI,
            PI   DANIEL R SOPPET,PAUL A MOORE,YANGGU SHI,DAVID W LAFLEUR,HENRIK

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ORIGIN

  Query Match             41.5%;  Score 505.4;  DB 6;  Length 2133;
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